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(54) Title: SUBTILISIN VARIANTS CAPABLE OF CLEAVING SUBSTRATES CONTAINING BASIC RESIDUES (57) Abstract <p>The bacterial serine protease, subtilisin BPN', has been mutated so that it will efficiently and selectively cleave substrates containing basic residues. Combination mutants, where Asn 62 was changed to Asp, Gly 166 was changed to Asp (N62D/G166D), and optionally Tyr 104 was changed to Asp had a larger than additive shift in specificity toward substrates containing basic residues. Suitable substrates of the subtilisin variants were revealed by sorting a library of phage particles (substrate phage) containing five contiguous randomized residues. This method identified a particularly good substrate, Asn-Leu-Met-Arg-Lys- (SEQ ID NO: 35), that was selectively cleaved in the context of a fusion protein by the N62D/G166D subtilisin variant. A particularly good substrate for N62D/G166D/Y104D would be Asn-Arg-Met-Arg-Lys- (SEQ ID NO: 76). Accordingly, these subtilisin variants are useful for cleaving fusion proteins with basic substrate linkers and processing hormones or other proteins <i>in vitro</i> or <i>in vivo</i> that contain basic cleavage sites.</p>			

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SUBTILISIN VARIANTS CAPABLE OF CLEAVING SUBSTRATES CONTAINING BASIC RESIDUES

FIELD OF THE INVENTION

This invention relates to subtilisin variants having altered specificity from wild-type subtilisins. Specifically, the subtilisin variants are modified so that they efficiently and selectively cleave substrates containing basic residues. The invention further relates to the DNA encoding these novel polypeptides, as well as the recombinant materials and methods for producing these subtilisin variants. In a particular aspect, the present invention provides for processes for cleaving protein substrates containing basic residues.

BACKGROUND OF THE INVENTION

Site-specific proteolysis is one of the most common forms of post-translational modifications of proteins (for review see Neurath, H. (1989) Trends Biochem. Sci., 14:268). In addition, proteolysis of fusion proteins *in vitro* is an important research and commercial tool (for reviews see Uhlen, M. and Moks, T. (1990) Methods Enzymol., 185:129-143; Carter, P. (1990) in Protein Purification: From Molecular Mechanisms to Large-Scale Processes, M.R. Landisch, R.C. Wilson, C.D. Painton, S.E. Builder, Eds. (ACS Symposium Series 427, American Chemical Society, Washington, D.C.), Chap. 13, p.181-193; and Nilsson, B. et al. (1992) Current Opin. Struct. Biol., 2:569). Expressing a protein of interest as a fusion protein facilitates purification when the fusion contains an affinity domain such as glutathione-S-transferase, Protein A or a poly-histidine tail. The fusion domain can also facilitate high level expression and/or secretion.

To liberate the protein product from the fusion domain requires selective and efficient cleavage of the fusion protein. Both chemical and enzymatic methods have been proposed (see references above). Enzymatic methods are generally preferred as they tend to be more specific and can be performed under mild conditions that avoid denaturation or unwanted chemical side-reactions. A number of natural and even designed enzymes have been applied for site-specific proteolysis. Although some are generally more useful than others (Forsberg, G., Baastrup, B., Rondahl, H., Holmgren, E., Pohl, G., Hartmanis, M. and Lake, M. (1992) J. Prot. Chem., 11:201-211), no one is applicable to every situation given the sequence requirements of the fusion protein junction and the possible existence of protease sequences within the desired protein product. Thus, an expanded array of sequence specific proteases, analogous to restriction endonucleases, would make site-specific proteolysis a more widely used method for processing fusion proteins or generating protein/peptide fragments either *in vitro* or *in vivo*.

The processing of prohormones by the KEX2-related family of serine endoproteases illustrates one of the most precise proteolytic events found in nature (for reviews see Steiner, D. F., Smeekens, S. P., Ohagi, S. and Chan, S. J. (1992) J. Biol. Chem., 267, 23435-23438 and Smeekens, S. P. (1993) Bio/Technology 11, 182-186). This family of proteases, that includes the yeast KEX2 and the mammalian PC2, PC3 and furin enzymes, are homologous to the bacterial serine protease subtilisin (Kraut, J. (1977) Annu. Rev. Biochem., 46:331-358). Subtilisin has a broad substrate specificity that reflects its role as a scavenger protease. In contrast, these eukaryotic enzymes are very specific for cleaving substrates containing two basic residues and thus well-suited for site-specific proteolysis.

All of these eucaryotic enzymes strongly require Arg at the P1 position, and either Arg, Lys or Pro at the P2 position of peptide substrates. The prohormone convertases from higher eukaryotes such as furin, PC2, and PC3 also have an absolute requirement for Arg at the P4 position (Bresnahan, P. A., Leduc, R., Thomas, L., Thomer, J., Gibson, H. L., Brake, A. J., Barr, P. J. and Thomas, G. (1990) *J. Cell. Biol.* 111, 2851; Wise, R. J., Baar, P. J., Wong, P. A., Kiefer, M. C., Brake, A. J., and Kaufman, R. J. (1990) *Proc. Natl. Acad. Sci. USA* 87, 9378-9382.; Hosaka, M., Nagahama, M., Kim, W.-S., Watanabe, T., Hatsuzakawa, K., Ikemizu, J., Murakami, K., and Nakayama, K. (1991) *J. Biol. Chem.* 266, 12127-12130.; Matthews, D. J., Goodman, L. J., Gorman, C. M., and Wells, J. A. (1994) *Protein Science* 3, 1197-1205).

Despite the very narrow specificity of the pro-hormone processing enzymes, in some cases they are capable of rapid cleavage of target sequences. For example, the k_{cat}/K_m ratio for KEX2 to cleave a good substrate (e.g. acetyl-pMYRK-MCA) is $1.1 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$ (Brenner, C., and Fuller, R.S. (1992) *Proc. Natl. Acad. Sci. USA* , 89:922-926) compared to 3×10^5 for subtilisin cleaving a good substrate (e.g. suc-AAPF-pNA) (Estell, D. A., Graycar, T. P., Miller, J. V., Powers, D. B., Burnier, J. P., Ng, P. G. and Wells, J.A. (1986) *Science*, 233:659-663).

However, the eukaryotic proteases are expressed in small amounts (Bravo, D. B., Gleason, J. B., Sanchez, R. I., Roth, R. A., and Fuller, R. S. (1994) *J. Biol. Chem.*, 269:25830-25837 and Matthews, D. J., Goodman, L. J., Gorman, C. M., and Wells, J. A. (1994) *Protein Science* , 3:1197-1205) making them impractical to apply presently to processing of fusion proteins *in vitro*. Subtilisin BPN' however, can be expressed in large amounts (Wells, J.A., Ferrari, E., Henner, D.J., Estell, D.A. and Chen, E.Y. (1983) *Nucl. Acids Res.*, 11:7911-7929)

Extensive protein engineering studies of subtilisin, and especially subtilisin BPN', have identified several residues in the S1 and S2 active site of the enzyme where amino acid substitutions lead to large changes in substrate specificity (Wells, J. A., and Estell, D.A., (1988) *Trends Biochem. Sci.*, 13:291-297; Carter, P., et al., (1989) *PROTEINS:Structure, Function, and Genetics*, 6:240-248). X-ray crystal structures of subtilisin containing bound transition state analogues (Wright, C. S., Alden, R. A. and Kraut, J. (1969) *Nature* , 221:235-242; McPhalen, C.A. and James, N.G. (1988) *Biochemistry*, 27:6582-6598; Bode, W., Papamokos, E., Musil, D., Seemueller, U. and Fritz, M. (1986) *EMBO J.*, 5:813-818; and Bott, R., Utsch, M., Kossiakoff, A., Graycar, T., Katz, B. and Power, S. (1988) *J. Biol. Chem.*, 263:7895-7906) can be used to locate active site residues that are in close proximity to side chains at key positions in substrate peptides (Wells, J.A., (1987) *Proc. Natl. Acad. Sci. USA* 84:1219-1223). Consideration of electrostatic interactions between charged peptide substrates and subtilisin can be used to tailor the substrate binding cleft of the subtilisin BPN' to favor complementary charged substrates (Wells, J.A., et al., (1987) *Proc. Natl. Acad. Sci., USA*, 84:1219-1223). Previous work has shown that replacement of residues at position 156 and 166 in the S1 binding site of subtilisin BPN' with various charged residues leads to improved specificity for complementary charged substrates.

A substantial amount of protein engineering has been applied to the specificity determinants of the S4 subsite of subtilisin BPN' in efforts to alter specificity for P4 substrates (Eder, J., Rheinhecker, M., and Fersht, A. R. (1993) *FEBS Lett* 335, 349-352; Rheinhecker, M., Baker, G., Eder, J., and Fersht, A. R. (1993) *Biochemistry* 32, 1199-1203; Rheinhecker, M., Eder, J., Pandey, P.S., and Fersht, A. R. (1994) *Biochemistry* 33,

221-225). However, the mutations introduced consisted entirely of hydrophobic substitutions, thus preserving the overall hydrophobic substrate preference in the site.

Previous attempts to introduce, remove or reverse charge specificity in enzyme active sites have been met with considerable difficulty. This has generally been attributed to a lack of stabilization of the introduced charge or enzyme-substrate ion pair complex by the wild-type enzyme environment (Hwang, J.K. and Warshel, A. (1988) *Nature*, 334:270-272). For example, Stennicke *et al* (Stennicke, H.R.; Ujje, H.M.; Christensen, U.; Remington, S.J.; and Breddam (1994) *Prot. Eng.* 7:911-916) made acidic (D/E) mutations at five residues in the P1' binding of carboxypeptidase Y in an attempt to change the P1' preference from Phe to Lys/Arg. Only the L272D and L272E mutations were found to alter the specificity in the desired direction, up to 1.5-fold preference in Lys/Arg over Phe, and the others simply resulted in less active enzymes having substrate preferences similar to wild-type. In the case of trypsin, a protease that is highly specific for basic P1 residues, recruitment of chymotrypsin-like (hydrophobic P1) specificity required not only mutations of the ion pair-forming Asp 189 to Ser, but also transplantation of two more distant surface loops from chymotrypsin (Graf, L., Jancso, A., Szilagyi, L., Hegyi, G., Pinter, K., Naray-Szabo, G., Hepp, J., Medzihradszky, K., and Rutter, W. J., *Proc. Natl. Acad. Sci. USA* (1988) 85:4961-4965 and Hedstrom, L., Szilagyi, L., and Rutter, W. J., *Science* (1992) 255:1249-1253).

In the present work, we have also verified that relatively low specificity is gained by introducing single ion-pairs between enzyme and substrate. However, when two or more choice ionic interactions were simultaneously engineered into subtilisin BPN', the resulting variants had higher specificity for basic residues in each of the subsites due to a non additive effect.

Accordingly, it is an object to produce a subtilisin variant with basic specificity for use in processing pro-proteins made by recombinant techniques.

SUMMARY OF THE INVENTION

The present invention provides for subtilisin variants with altered substrate specificity. Preferred subtilisin variants are highly specific for the efficient cleavage of substrates containing basic residues. The subtilisin variants have a substrate specificity which is substantially different from the substrate specificity of the precursor subtilisin from which the amino acid sequence of the variant is derived. The amino acid sequence of the subtilisin variants are derived by the substitution of one or more amino acids of a precursor subtilisin amino acid sequence.

In a preferred aspect of the present invention, the subtilisin variants of the present invention are specific for the cleavage of protein substrates containing basic amino acid residues at substrate positions P1, P2 and P4. According to this aspect of the present invention subtilisin variants having amino acid substitutions at positions corresponding to amino acid positions 62, 104 and 166 of subtilisin BPN' produced by *Bacillus amyloliquefaciens* are preferred. Accordingly, subtilisin variants are provided wherein amino acids 62, 104 and 166 of subtilisin BPN' are substituted with an acidic amino acids. Preferably the acidic amino acid is Asp or Glu, and most preferably Asp.

Preferred substrates for the subtilisin variants according to this aspect of the present invention contain either Lys (K) or Arg (R) at substrate positions P2 and P1, practically any residue at P3, and preferably either Lys or Arg at P4, and again practically any residue at P5. Thus an exemplary good substrate would contain -Asn-Arg-Met-Arg-Lys- (SEQ ID NO: 76) at -P5-P4-P3-P2-P1- respectively. Additionally, good substrates would not have Pro at P1', P2', or P3' nor would Ile be present at P1'.

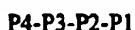
According to a second aspect of the present invention the subtilisin variants are capable of cleaving protein substrates having basic residues at positions P1 and P2. According to this aspect of the present invention subtilisin variants having amino acid substitutions at positions corresponding to amino acid positions 62, and 166 of subtilisin BPN' produced by *Bacillus amyloliquefaciens* are preferred. The preferred subtilisin variants having substrate specificity for dibasic substrates have an acidic amino acid residue at residue position 62 of subtilisin naturally produced by *Bacillus amyloliquefaciens*. In a preferred embodiment, the naturally occurring Asn at residue position 62 of subtilisin BPN' is preferably substituted with an acidic amino acid residue such as Glu or Asp, and most preferably Asp. The preferred subtilisin variants, having substrate specificity for substrates having dibasic amino acid residues, additionally have an acidic residue, Asp or Glu, at residue position 166 of subtilisin BPN'. Thus, the subtilisin BPN' variant containing substitution of amino acids 62 and 166 with acidic amino acids Glu or Asp are preferred. In particular, a subtilisin variant having amino acid Asp at positions 62 and 166 is preferred (subtilisin BPN' variant N62D/G166D). The subtilisin variants according to this aspect of the invention may be used to cleave substrates containing dibasic residues such as fusion proteins with dibasic substrate linkers and processing hormones or other proteins (*in vitro* or *in vivo*) that contain dibasic cleavage sites.

Preferred substrates for the subtilisin BPN' variant N62D/G166D contain either Lys (K) or Arg (R) at substrate positions P2 and P1, practically any residue at P3, a non-charged hydrophobic residue at P4, and again practically any residue at P5. Thus an exemplary good substrate would contain -Asn-Leu-Met-Arg-Lys- (SEQ ID NO: 35) at -P5-P4-P3-P2-P1- respectively. Additionally, good substrates would not have Pro at P1', P2', or P3' nor would Ile be present at P1'.

The invention also includes mutant DNA sequences encoding such subtilisin variants. These mutant DNA sequences are derived from a precursor DNA sequence which encodes a naturally occurring or recombinant precursor subtilisin. The mutant DNA sequence is derived by modifying the precursor DNA sequence to encode the substitution(s) of one or more amino acids encoded by the precursor DNA sequence. These recombinant DNA sequences encode mutants having an amino acid sequence which does not exist in nature and a substrate specificity which is substantially different from the substrate specificity of the precursor subtilisin encoded by the precursor DNA sequence.

Further the invention includes expression vectors containing such mutant DNA sequences as well as host cells transformed with such vectors which are capable of expressing the subtilisin variants.

The invention also provides for a process for cleaving a polypeptide such as a fusion protein containing a substrate linker represented by the formula:



wherein P4 is a basic amino acid or a large hydrophobic amino acid such as Leu or Met; P3 is an amino acid selected from the naturally occurring amino acids; P2 is a basic amino acid; and P1 is a basic amino acid. The

process includes the step of subjecting the polypeptide to the subtilisin variants described herein under conditions such that the subtilisin variant cleaves the polypeptide.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Structure of a succinyl-Ala-Ala-Pro-BoroPhe (SEQ ID NO: 69) inhibitor bound to the active site of subtilisin BPN' showing the S2 and S1 binding pocket residues subjected to mutagenesis.

Figure 2. Kinetic analysis of S1 binding site subtilisin mutants versus substrates having variable P1 residues. The kinetic constant k_{cat}/K_m was determined from plots of initial rates versus substrate concentration for the tetrapeptide series succinyl-Ala-Ala-Pro-Xaa-pNa (SEQ ID NO: 69), where Xaa was Lys (SEQ ID NO: 58), Arg (SEQ ID NO: 59), Phe (SEQ ID NO: 56), Met (SEQ ID NO: 60) or Gln (SEQ ID NO: 61) (defined to the right of the plot).

Figure 3. Kinetic analysis of S2 binding site subtilisin mutants versus substrates having variable P2 residues. The kinetic constant k_{cat}/K_m was determined from plots of initial rates versus substrate concentration for the tetrapeptide series succinyl-Ala-Ala-Xaa-Phe-pNa (SEQ ID NO: 70), where Xaa was Lys (SEQ ID NO: 62), Arg (SEQ ID NO: 64), Ala (SEQ ID NO: 63), Pro (SEQ ID NO: 56), or Asp (SEQ ID NO: 65) (defined on the right of the plot).

Figure 4. Kinetic analysis of combined S1 and S2 binding site subtilisin mutants versus substrates having variable P1 and P2 residues. The kinetic constants k_{cat}/K_m were determined from plots of initial rates versus substrate concentration for the tetrapeptide series succinyl-Ala-Ala-Xaa₂-Xaa₁-pNa (SEQ ID NO: 71), where Xaa₂-Xaa₁ was Lys-Lys (SEQ ID NO: 66), Lys-Arg (SEQ ID NO: 67), Lys-Phe (SEQ ID NO: 62), Pro-Lys (SEQ ID NO: 58), Pro-Phe (SEQ ID NO: 56), or Ala-Phe (SEQ ID NO: 63) (defined on the right of the plot).

Figure 5. Results of hGH-AP fusion protein assay. hGH-AP fusion proteins were constructed, bound to hGHbp-coupled resin, and treated with 0.5 nM N62D/G166D subtilisin in 20 mM Tris-Cl pH 8.2. Aliquots were withdrawn at various times and AP release was monitored by activity assay in comparison to a standard curve. Arrows indicate the cleavage site. The rate of cleavage of fusion proteins containing various substrate linkers is shown. Substrates containing a Pro at position P1' are not cleaved.

Figure 6-1 - 6-10. (Collectively referred to herein as Fig. 6). DNA sequence of the phagemid pSS5 containing the N62D/G166D double mutant subtilisin BPN' gene (SEQ ID NO: 1), and translated amino acid sequence for the mutant preprosubtilisin (SEQ ID NO: 2). The pre region is comprised of residues -107 to -78, the pro of residues -77 to -1, and the mature enzyme of residues +1 to +275 (SEQ ID NO: 72). Also shown are restriction sites recognized by endonucleases that require 6 or more specific bases in succession.

Figure 7. Structure of a succinyl-Ala-Ala-Pro-BoroPhe (SEQ ID NO: 69) inhibitor bound to the active site of subtilisin BPN' showing the S1, S2, and S4 binding pocket residues subjected to mutagenesis.

Figure 8. DNA sequence of the N62D/Y104D/G166D triple mutant (SEQ ID NO: 74) as well as the translated amino acid sequence (SEQ ID NO: 75). The preregion is comprised of residues -107 to -78, the pro residues -77 to -1 and the mature enzyme +1 to +275. The proregion reflects the changes, A(-4)R/A(-2)K/Y(-1)R made in the wild-type processing site to affect expression.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

Terms used in the claims and specification are defined as set forth below unless otherwise specified.

The term amino acid or amino acid residue, as used herein, refers to naturally occurring L amino acids or residues, unless otherwise specifically indicated. The commonly used one- and three-letter abbreviations for amino acids are use herein (Lehninger, A. L., *Biochemistry*, 2d ed., pp. 71-92, Worth Publishers, N. Y. (1975)). Basic amino acids are Arg and Lys. Acidic amino acids are Asp and Glu.

Substrates are described in triplet or single letter code as Pn...P2-P1-P1'-P2'...Pn'. The "P1" residue refers to the position proceeding (i.e., N-terminal to) the scissile peptide bond (i.e. between the P1 and P1' residues) of the substrate as defined by Schechter and Berger (Schechter, I. and Berger, A., *Biochem. Biophys. Res. Commun.* 27: 157-162 (1967)). Similarly, the term P1' is used to refer to the position following (i.e., C-terminal to) the scissile peptide bond of the substrate. Increasing numbers refer to the next consecutive position preceding (e.g., P2 and P3) and following (e.g., P2' and P3') the scissile bond. According to the present invention the scissile peptide bond is that bond that is cleaved by the subtilisin variants of the instant invention.

"Subtilisins," "precursor subtilisin" and the like are bacterial carbonyl hydrolases which generally act to cleave peptide bonds of proteins or peptides. As used herein, "subtilisin" means a naturally occurring subtilisin or a recombinant subtilisin. A series of naturally occurring subtilisins are known to be produced and often secreted by various bacterial species (Siezen, R.J., et al., (1991) *Protein Engineering* 4:719-737). Amino acid sequences of the members of this series are not entirely homologous. However, the subtilisins in this series exhibit the same or similar type of proteolytic activity. This class of serine proteases shares a common amino acid sequence defining a catalytic triad which distinguishes them from the chymotrypsin related class of serine proteases. The subtilisins and chymotrypsin related serine proteases both have a catalytic triad comprising aspartate, histidine and serine. In the subtilisin related proteases the relative order of these amino acids, reading from the amino to carboxy terminus is aspartate-histidine-serine. In the chymotrypsin related proteases the relative order, however is histidine-aspartate-serine. Thus, subtilisins as used herein refer to a serine protease having the catalytic triad of subtilisin related proteases.

Generally, subtilisins are serine endoproteases having molecular weights of about 27,500 which are secreted in large amounts from a wide variety of *Bacillus* species. The protein sequence of subtilisins have been determined from at least four different species of *Bacillus* (Markland, F.S., et al. (1971) in *The Enzymes*, ed. Boyer P.D., Acad Press, New York, Vol. III, pp. 561-608; and Nedkov, P. et al. (1983) *Hoppe-Seyler's Z. Physiol. Chem.* 364:1537-1540). The three-dimensional crystallographic structure of four subtilisins have been reported (BPN' from *Bacillus amyloliquefaciens*, Hirono et al. (1984) *J. Mol. Biol.* 178:389-413; subtilisin Carlesberg from *Bacillus licheniformis*, Bode et al., (1986) *EMBO J.* 5:813-818; thermolysin from *Thermoplasma acidophilum*, Gros et al., (1989) *J. Mol. Biol.* 210:347-367; and proteinase K from *Tritirachium album*, Betzel, et al., (1988) *Acta Crystallogr., B*, 44:163-172). The three dimensional structure of subtilisin BPN' (from *B. amyloliquefaciens*) to 2.5Å resolution has also been reported by Wright, C.S. et al. (1969) *Nature* 221:235-242 and Drenth, J. et al. (1972) *Eur. J. Biochem.* 26:177-181. These studies indicate that although subtilisin is genetically unrelated to the mammalian serine proteases, it has a similar fold and active site structure. The x-ray crystal structures of subtilisin containing covalently bound peptide inhibitors (Robertus, J.D., et al.

(1972) *Biochemistry* 11:2439-2449), product complexes (Robertus, J.D., et al. (1972) *Biochemistry* 11:4293-4303), and transition state analogs (Matthews, D.A., et al. (1975) *J. Biol. Chem.* 250:7120-7126 and Poulos, T.L., et al. (1976) *J. Biol. Chem.* 251:1097-1103), which have been reported have also provided information regarding the active site and putative substrate binding cleft of subtilisins. In addition, a large number of kinetic and chemical modification studies have been reported for subtilisins (Phillip, M., et al. (1983) *Mol. Cell. Biochem.* 51:5-32; Svendsen, I.B. (1976) *Carlsberg Res. Comm.* 41:237-291 and Markland, F.S. *Id.*) as well as at least one report wherein the side chain of methionine at residue 222 of subtilisin was converted by hydrogen peroxide to methionine-sulfoxide (Stauffer, D.C., et al. (1965) *J. Biol. Chem.* 244 5333-5338).

"Subtilisin variant," "subtilisin mutant" and the like refer to a subtilisin-type serine protease having a sequence which is not found in nature that is derived from a precursor subtilisin according to the present invention. The subtilisin variant has a substrate specificity different from the precursor subtilisin by virtue of amino acid substitutions within the precursor subtilisin amino acid sequence. The term is meant to include subtilisin variants in which the DNA sequence encoding the precursor subtilisin is modified to produce a mutant DNA sequence which encodes the substitution of one or more amino acids in the naturally occurring subtilisin amino acid sequence. Suitable methods to produce such modification include those disclosed in U. S. Patent No. 4,760,025 and 5,371,008 and in EPO Publication No. 0130756 and 0251446.

A change in substrate specificity is defined as a difference between the K_{cat}/K_m ratio of the precursor subtilisin and the subtilisin variant. The K_{cat}/K_m ratio is a measure of catalytic efficiency. Subtilisin variants with increased or decreased K_{cat}/K_m ratios compared to the precursor subtilisin from which they were derived are described herein. Generally, the objective is to secure a variant having a greater, i.e. numerically larger, K_{cat}/K_m ratio for a given substrate. A greater K_{cat}/K_m ratio for a particular substrate indicates that the variant may be used to more efficiently cleave the target substrate.

The specificity or discrimination between two or more competing substrates is determined by the ratios of k_{cat}/K_m (Fersht, A.R., (1985) in *Enzyme Structure and Mechanism*, W.F. Freeman and Co., N.Y. p. 112). An increase in K_{cat}/K_m ratio for one substrate may be accompanied by a reduction in K_{cat}/K_m ratio for another substrate. This shift in substrate specificity indicates that the variant subtilisin with the increased K_{cat}/K_m ratio for the substrate has utility in cleaving the particular substrate over the precursor subtilisin in, for example, preventing undesirable hydrolysis of a particular substrate in a mixture of substrates.

In general, for a subtilisin variant to have a useful catalytic efficiency for cleavage of a particular substrate the K_{cat}/K_m ratio will generally be between $1 \times 10^3 \text{ M}^{-1} \text{ s}^{-1}$ to about $1 \times 10^7 \text{ M}^{-1} \text{ s}^{-1}$. More often, the K_{cat}/K_m ratio will be between about $1 \times 10^4 \text{ M}^{-1} \text{ s}^{-1}$ and $1 \times 10^6 \text{ M}^{-1} \text{ s}^{-1}$.

When referring to mutants or variants, the wild type amino acid residue is followed by the residue number and the new or substituted amino acid residue. For example, substitution of D for wild type N in residue position 62 is denominated N62D.

"Subtilisin variants or mutants" are designated in the same manner by using the single letter amino acid code for the wild-type residue followed by its position and the single letter amino acid code of the replacement residue. Multiple mutants are indicated by component single mutants separated by slashes. Thus the subtilisin BPN' variant N62D/G166D is a di-substituted variant in which Asp replaces Asn and Gly at residue positions 62 and 166, respectively, in wild-type subtilisin BPN'.

An amino acid residue of a precursor carbonyl hydrolase is "equivalent" to a residue of *B. amyloliquefaciens* subtilisin if it is either homologous (i.e., corresponding in position in either primary or tertiary structure) or analogous to a specific residue or portion of that residue in *B. amyloliquefaciens* subtilisin (i.e., having the same or similar functional capacity to combine, react, or interact chemically).

5 In order to establish homology to primary structure, the amino acid sequence of a precursor carbonyl hydrolase is directly compared to the *B. amyloliquefaciens* subtilisin primary sequence and particularly to a set of residues known to be invariant in all subtilisins for which the sequences are known (see e.g. Figure 5-C in EPO 0251446). After aligning the conserved residues, allowing for necessary insertions and deletions in order to maintain alignment (i.e., avoiding the elimination of conserved residues through arbitrary deletion and insertion),
 10 the residues equivalent to particular amino acids in the primary sequence of *B. amyloliquefaciens* subtilisin are defined. Alignment of conserved residues should conserve 100% of such residues. However, alignment of greater than 75% or as little as 50% of conserved residues is also adequate to define equivalent residues. Conservation of the catalytic triad, Asp32/His64/Ser221, is required.

Equivalent residues homologous at the level of tertiary structure for a precursor carbonyl hydrolase whose
 15 tertiary structure has been determined by x-ray crystallography, are defined as those for which the atomic coordinates of 2 or more of the main chain atoms of a particular amino acid residue of the precursor carbonyl hydrolase and *B. amyloliquefaciens* subtilisin (N on N, CA on CA, C on C, and O on O) are within 0.13nm and preferably 0.1nm after alignment. Alignment is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the carbonyl hydrolase
 20 in question to the *B. amyloliquefaciens* subtilisin. The best model is the crystallographic model giving the lowest R factor for experimental diffraction data at the highest resolution available.

$$R \text{ factor} = \frac{\sum_h |F_o(h)| - |F_c(h)|}{\sum_h |F_o(h)|}$$

Equivalent amino acid residues of subtilisin BPN⁺, subtilisin Carlsberg, thermitase and proteinase K from tertiary structure analysis is provided in, for example, Siezen, et al., (1991) Prot. Eng. 4:719-737.

30 Equivalent residues which are functionally analogous to a specific residue of *B. amyloliquefaciens* subtilisin are defined as those amino acids of the precursor carbonyl hydrolases which may adopt a conformation such that they either alter, modify or contribute to protein structure, substrate binding or catalysis in a manner defined and attributed to a specific residue of the *B. amyloliquefaciens* subtilisin as described herein. Further, they are those residues of the precursor carbonyl hydrolase (for which a tertiary structure has been obtained by
 35 x-ray crystallography), which occupy an analogous position to the extent that although the main chain atoms of the given residue may not satisfy the criteria of equivalence on the basis of occupying a homologous position, the atomic coordinates of at least two of the side chain atoms of the residue lie within 0.13nm of the

corresponding side chain atoms of *B. amyloliquefaciens* subtilisin. The three dimensional structures would be aligned as outlined above.

Some of the residues identified for substitution are conserved residues whereas others are not. In the case of residues which are not conserved, the replacement of one or more amino acids is limited to substitutions which produce a mutant which has an amino acid sequence that does not correspond to one found in nature. In the case of conserved residues, such replacements should not result in a naturally occurring sequence. The subtilisin mutants of the present invention include the mature forms of subtilisin mutants as well as the pro- and prepro-forms of such subtilisin mutants. The prepro-forms are the preferred construction since this facilitates the expression, secretion and maturation of the subtilisin mutants.

10 "Prosequence" refers to a sequence of amino acids bound to the N-terminal portion of the mature form of a subtilisin which when removed results in the appearance of the "mature" form of the subtilisin. Many proteolytic enzymes are found in nature as translational proenzyme products and, in the absence of post-translational processing, are expressed in this fashion. The preferred prosequence for producing subtilisin mutants, specifically subtilisin BPN' mutants, is the putative prosequence of *B. amyloliquefaciens* subtilisin although other subtilisin prosequences may be used. For example, when the substrate specificity of the precursor subtilisin is altered according to the present invention, this alteration may affect the ability of the variant subtilisin to undergo autolytic cleavage of the naturally occurring prosequence. In order to affect the expression and proper folding of a mature variant subtilisin whose substrate specificity has been altered, it may be necessary to alter the prosequence to correspond to the new or variant substrate specificity.

20 As an example, the substrate specificity of a particular subtilisin variant N62D/Y104D/G166D is distinct from the precursor subtilisin from which it was derived. The subtilisin variant prefers substrates containing basic residues at substrate positions corresponding to P4, P2, and P1. According to this aspect of the present invention, the precursor prosequence which was efficiently autolysed by the precursor subtilisin is altered to correspond to the substrate specificity of the variant subtilisin. Therefore, for the subtilisin variant N62D/Y104/G166D the prosequence would be altered to contain basic residues at positions -4, -2, and -1.

25 A "signal sequence" or "presequence" refers to any sequence of amino acids bound to the N-terminal portion of a subtilisin or to the N-terminal portion of a prosubtilisin which may participate in the secretion of the mature or pro forms of the subtilisin. This definition of signal sequence is a functional one, meant to include all those amino acid sequences, encoded by the N-terminal portion of the subtilisin gene or other secretory carbonyl hydrolases, which participate in the effectuation of the secretion of subtilisin or other carbonyl hydrolases under native conditions. The present invention utilizes such sequences to effect the secretion of the subtilisin mutants as defined herein.

30 A "prepro" form of a subtilisin mutant consists of the mature form of the subtilisin having a prosequence operably linked to the amino-terminus of the subtilisin and a "pre" or "signal" sequence operably linked to the amino terminus of the prosequence.

"Expression vector" refers to a DNA construct containing a DNA sequence which is operably linked to a suitable control sequence capable of effecting the expression of the DNA in a suitable host. Such control sequences include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome binding sites, and sequences which control termination of

transcription and translation. The vector may be a plasmid, a phage particle, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the present specification, "plasmid" and "vector" are sometimes used interchangeably as the plasmid is the most commonly used form of vector at present.

5 However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which are, or become, known in the art.

The "host cells" used in the present invention generally are procaryotic or eucaryotic hosts which preferably have been manipulated by the methods disclosed in EPO Publication No. 0130756 or 0251446 or U.S. Patent No. 5,371,008 to render them incapable of secreting enzymatically active endoprotease. A preferred host
10 cell for expressing subtilisin is the *Bacillus* strain BG2036 which is deficient in enzymatically active neutral protease and alkaline protease (subtilisin). The construction of strain BG2036 is described in detail in EPO Publication No. 0130756 and further described by Yang, M.Y., *et al.* (1984) *J. Bacteriol.* 160:15-21. Such host cells are distinguishable from those disclosed in PCT Publication No. 03949 wherein enzymatically inactive mutants of intracellular proteases in *E. coli* are disclosed. Other host cells for expressing subtilisin include
15 *Bacillus subtilis* var. I168 (EPO Publication No. 0130756).

Host cells are transformed or transfected with vectors constructed using recombinant DNA techniques. Such transformed host cells are capable of either replicating vectors encoding the subtilisin mutants or expressing the desired subtilisin mutant. In the case of vectors which encode the pre or prepro form of the subtilisin mutant, such mutants, when expressed, are typically secreted from the host cell into the host cell medium.

20 "Operably linked" when describing the relationship between two DNA regions simply means that they are functionally related to each other. For example, a presequence is operably linked to a peptide if it functions as a signal sequence, participating in the secretion of the mature form of the protein most probably involving cleavage of the signal sequence. A promoter is operably linked to a coding sequence if it controls the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned
25 so as to permit translation.

The genes encoding the naturally-occurring precursor subtilisin may be obtained in accord with the general methods described in U.S. Patent No. 4,760,025 or EPO Publication No. 0130756. As can be seen from the examples disclosed therein, the methods generally comprise synthesizing labeled probes having putative sequences encoding regions of the hydrolase of interest, preparing genomic libraries from organisms expressing
30 the hydrolase, and screening the libraries for the gene of interest by hybridization to the probes. Positively hybridizing clones are then mapped and sequenced.

The cloned subtilisin is then used to transform a host cell in order to express the subtilisin. The subtilisin gene is then ligated into a high copy number plasmid. This plasmid replicates in hosts in the sense that it contains the well-known elements necessary for plasmid replication: a promoter operably linked to the gene in question
35 (which may be supplied as the gene's own homologous promotor if it is recognized, *i.e.*, transcribed, by the host), a transcription termination and polyadenylation region (necessary for stability of the mRNA transcribed by the host from the hydrolase gene in certain eucaryotic host cells) which is exogenous or is supplied by the endogenous terminator region of the subtilisin gene and, desirably, a selection gene such as an antibiotic resistance gene that enables continuous cultural maintenance of plasmid-infected host cells by growth in

antibiotic-containing media. High copy number plasmids also contain an origin of replication for the host, thereby enabling large numbers of plasmids to be generated in the cytoplasm without chromosomal limitations. However, it is within the scope herein to integrate multiple copies of the subtilisin gene into host genome. This is facilitated by procaryotic and eucaryotic organisms which are particularly susceptible to homologous recombination.

Once the subtilisin gene has been cloned, a number of modifications are undertaken to enhance the use of the gene beyond synthesis of the naturally-occurring precursor subtilisin. Such modifications include the production of recombinant subtilisin as disclosed in U.S. Patent No. 5,371,008 or EPO Publication No. 0130756 and the production of subtilisin mutants described herein.

10 *Mutant design and preparation.*

A. Subtilisin Variants Capable of Cleaving Substrates Having Dibasic Residues.

For the preparation of subtilisin variants capable of cleaving substrates containing dibasic residues, the following analysis was undertaken.

A number of structures have been solved of subtilisin with a variety of inhibitors and transition state analogs bound (Wright, C. S., Alden, R. A. and Kraut, J. (1969) *Nature*, 221:235-242; McPhalen, C.A. and James, N.G. (1988) *Biochemistry*, 27:6582-6598; Bode, W., Papamokos, E., Musil, D., Seemueller, U. and Fritz, M. (1986) *EMBO J.*, 5:813-818; and Bott, R., Ultsch, M., Kossiakoff, A., Graycar, T., Katz, B. and Power, S. (1988) *J. Biol. Chem.*, 263:7895-7906). One of these structures, Figure 1, was used to locate residues that are in close proximity to side chains at the P1 and P2 positions from the substrate. Previous work had shown that replacement residues at positions 156 and 166 in the S1 binding site with various charged residues lead to improved specificity for complementary charged substrates (Wells, J. A., Powers, D. B., Bott, R. R., Graycar, T. P. and Estell, D. A. (1987) *Proc. Natl. Acad. Sci. USA*, 84:1219-1223). Although longer range electrostatic effects of substrate specificity have been noted (Russell, A. J. and Fersht, A. R. (1987) *Nature*, 328:496-500) these were generally much smaller than local ones. Therefore, it seemed reasonable that local differences in charge between subtilisin BPN' and the eukaryotic enzymes may account for the differences in specificity.

A detailed sequence alignment of 35 different subtilisin-like enzymes (Siezen, R. J., de Vos, W. M., Leunissen, A. M., and Dijkstra, B. W. (1991) *Prot. Eng.*, 4:719-737) allowed us to identify differences between subtilisin BPN' and the eukaryotic processing enzymes, KEX2, furin and PC2. Within the S1 binding pocket there are a number of charged residues that appear in the pro-hormone processing enzymes and not in subtilisin BPN' (Table 1A).

TABLE 1A*S1 subste*

	125-131 ^a	151-157	163-168
Subtilisin BPN'	S L G G P S G (SEQ ID NO: 3)	A A A G N E G (SEQ ID NO: 4)	S T - V G Y P (SEQ ID NO: 5)
Kex2	S W G P A D D (SEQ ID NO: 6)	F A S G N G G (SEQ ID NO: 7)	C N Y D G Y T (SEQ ID NO: 8)
Furin	S W G P E D D (SEQ ID NO: 9)	W A S G N G G (SEQ ID NO: 10)	C N C D G Y T (SEQ ID NO: 11)
PC2	S W G P A D D (SEQ ID NO: 6)	W A S G D G G (SEQ ID NO: 12)	C N C D G Y A (SEQ ID NO: 13)

^a numbering according to subtilisin BPN' sequence

For example, the eukaryotic enzymes have two conserved Asp residues at 130 and 131 as well as an Asp at 165 that is preceded by insertion of a Tyr or Cys. However, in the region from 151-157, subtilisin BPN' contains a Glu and the eukaryotes a conserved Gly.

In the S2 binding site there were two notable differences in sequence (Table 1B).

TABLE 1B*S2 subste*

	30-35	60-64
Subtilisin BPN'	V I D S G I (SEQ ID NO: 14)	D N N S H (SEQ ID NO: 15)
KEX2	I V D D G L (SEQ ID NO: 16)	S D D Y H (SEQ ID NO: 17)
Furin	I L D D G I (SEQ ID NO: 18)	N D N R H (SEQ ID NO: 19)
PC2	I M D D G I (SEQ ID NO: 20)	W F N S H (SEQ ID NO: 21)

Subtilisin BPN' contains a Ser at position 33 whereas the pro-hormone processing enzymes contain Asp. There is not as clear a consensus in the region of 60-64, but one notable difference is at position 62. This side chain which points directly at the P2 side chain (Figure 1) is Asn in subtilisin BPN', furin and PC2 but Asp in KEX2. Thus, not all substitutions were clearly predictive of the specificity differences.

A variety of mutants were produced to probe and engineer the specificity of subtilisin BPN' using oligonucleotides described in Table 2.

TABLE 2
*Oligonucleotides used for site-directed
mutagenesis on subtilisin.*

	Mutant	Oligonucleotide	Specificity Pocket	Activity Expressed
5	S33D	5'- GCGGTTATCGACG*A*CGGTATCGATTCT -3' (SEQ ID NO: 22)	S2	+
	S33K	5'- GCGGTTATCGACAA*A*G*GTATCGATTCT -3' (SEQ ID NO: 23)	S2	+
	S33E	5'- GCGGTTATCGACG*A*A*GGTATCGATTCT -3' (SEQ ID NO: 24)	S2	+
	N62D	5'- CCAAGACAACG*ACTCTCACGGAA -3' (SEQ ID NO: 25)	S2	+
	N62S	5'- CCAAGACAACAG*CTCTCACGGAA -3' (SEQ ID NO: 26)	S2	+
10	N62K	5'- CCAAGACAACAAA*TCTCACGGAA -3' (SEQ ID NO: 27)	S2	+
	G166D	5'-CACTTCCGGCAGCTCG*T*C*G*ACAGTGA*C*T ACCCTGGC.AAATA-3' (SEQ ID NO: 28) (Inserts Sal I site)	S1	+
	G166E	5'-CACTTCCGGCAGCTCG*T*C*G*ACAGTGA*GT ACCCTGGCAAATA-3' (SEQ ID NO: 29) (Inserts Sal I site)	S1	+
	G128P/P129A	5'- TTAACATGAGCCTCGGCC*C*AG*CTA*G*C*GGT TCTGCTGCTTTA -3' (SEQ ID NO: 30) (Inserts Nhe I site)	S1	-
15	G128P/P129A/ S130D/G131D	5'- TTAACATGAGCCTCGGCC*C*C*G*CGG*A*TGA* TTCTGCTGCTTTAAA -3' (SEQ ID NO: 31) (Inserts Sac II site)	S1	-
	T164N/V165D	5'-CGGCAGCTCAAGCA*A*C*G*A*T*GGCTAT*CCT GGCAAATACCCTTCTGTCA -3' (SEQ ID NO: 32) (Inserts BsaBI site)	S1	-

5	T164Y/V165D	5'-CGGCAGCTCAAGCA*A*C*G*A*T*GGCTAT*CCT GGCAAATACCCTTCTGTCA -3' (SEQ ID NO: 33) (Inserts BsaBI site)	S1	-
	T164N- Y(insert)- V165D	5'-ACTTCCGGCAGCTCT*T*C*G*AA*C*T*A*C*G*A* C*GGGTACCCTGGCAAATA-3' (SEQ ID NO: 34) (Inserts BstBI site)	S1	-
	N62D/G166D	See individual mutations	S1/S2	+
	N62D/G166E	See individual mutations	S1/S2	+

* Asterisks indicate base changes from the pSS5 (wild-type) template.

After producing the mutant plasmids they were transformed into a protease deficient strain of *B. subtilis* (BG2036) that lacks an endogenous gene for secretion of subtilisin. These were then tested for protease activity on skim milk plates.

The first set of mutants tested were ones where segments of the S1 binding site were replaced with sequences from KEX2. None of these segment replacements produced detectable activity on skim milk plates even though variants of subtilisin whose catalytic efficiencies are reduced by as much as 1000-fold do produce detectable halos (Wells, J.A., Cunningham, B.C., Graycar, T.P. and Estell, D.A. (1986) *Philos. Trans. R. Soc. Lond. A* . 317:415-423). We went on to produce single residue substitutions that should have less impact on the stability. These mutants at positions 166 in the S1 site, and 33 and 62 in the S2 site, were chosen based on the modeling and sequence considerations described above. Fortunately all single mutants as well as combination mutants produced activity on skim milk plates and could be purified to homogeneity.

20 *Kinetic analysis of variant subtilisins.*

To probe the effects of the G166E and G166D on specificity at the P1 position we used substrates having the form suc-AAPX-pna (SEQ ID NO: 69) where X was either Lys (SEQ ID NO. 58), Arg (SEQ ID NO. 59), Phe (SEQ ID NO. 56), Met (SEQ ID NO. 60) or Gln (SEQ ID NO. 61). The k_{cat}/K_m values were determined from initial rate measurements and results reported in Figure 2. Whereas the wild-type enzyme preferred Phe>Met>Lys>Arg>Gln, the G166E preferred Lys~Phe>Arg~Met>Gln, and G166D preferred Lys>Phe~Arg~Met>Gln. Thus, both the acidic substitutions at position 166 caused a shift in preference for basic residues at the P1 site, as previously reported (Wells, J. A., Powers, D. B., Bott, R. R., Graycar, T. P. and Estell, D. A. (1987a), *Proc. Natl. Acad. Sci. USA* 84:1219-1223).

The effects of single and double substitutions in the S2 binding site were analyzed with substrates having the form, suc-Ala-Ala-Xaa-Phe-pna (SEQ ID NO. 70) and are shown in Figure 3. At the P2 position the wild-type enzyme preferred Ala>Pro>Lys>Arg>Asp. In contrast, the S33D preferred Ala>Lys~Arg~Pro>Asp and the N62D preferred Lys>Ala>Arg>Pro>Asp. Although the effects were more dramatic for the N62D mutant, the S33D variant also showed significant improvement toward basic P2 residues and corresponding reduction

in hydrolysis of the Ala and Asp P2 substrates. We then analyzed the double mutant, but found it exhibited the catalytic efficiency of the worse of the two single mutants for each of the substrates tested.

Despite the less than additive effects seen for the two charged substitutions in the S2 site, we decided to combine the best S2 site variant (N62D) with either of the acidic substitutions in the S1 site. The two double mutants, N62D/G166E and N62D/G166D, were analyzed with substrates having the form, suc-AAXX-pna (SEQ ID NO. 71) where XX was either KK (SEQ ID NO. 66), KR (SEQ ID NO. 67), KF (SEQ ID NO. 62), PK (SEQ ID NO. 58), PF (SEQ ID NO. 56) or AF (SEQ ID NO. 63) (Figure 4). The wild-type preference was AF>PF>KF>KK>PK>KR, whereas the double mutants had the preference KK>KR>KF>PK>AF>PF. Thus for the double mutants there was a dramatic improvement toward cleavage of dibasic substrates and away from cleaving the hydrophobic substrates.

The greater than additive effect (or synergy) of these mutants can be seen from ratios of the catalytic efficiencies for the single and multiple mutants. For example, the G166E variant cannot distinguish Lys from Phe at the P1 position. Yet the N62D/G166E variant cleaves the Lys-Lys substrate about 8 times faster than the Lys-Phe substrate. Similarly the G166D cleaves the Lys P1 substrate about 3 times faster than the Phe P1 substrate, but the N62D/G166D double mutant cleaves a Lys-Lys substrate 18 times faster than a Lys-Phe substrate. Thus, as opposed to the reduction in specificity seen for the double mutant in the S2 site, the S1-S2 double mutants enhance specificity for basic residues. It is possible that these two sites bind the dibasic substrates in a cooperative manner analogous to a chelate effect.

Therefore, according to the present invention, subtilisin mutants having a preference for dibasic residues are preferred. According to this aspect of the present invention substitution of amino acids corresponding to amino acids N62 and G166 of subtilisin BPN' produced from *Bacillus amyloliquefaciens* are prepared. In particular, amino acids 62 and 166, or their equivalents, in the precursor subtilisin are substituted with amino acid residues Asp or Glu. Preferred subtilisin variants according to this aspect of the invention include N62D/G166D, N62E/G166E, N62E/G166D, and N62D/G166E variants of subtilisin BPN' and their equivalents.

25 B. Subtilisin Variants Capable of Cleaving Substrates Having Tribasic Residues

For the preparation of subtilisin variants specific for substrates containing a third basic residue at substrate position P4 we used the crystal structure of subtilisin BPN' complexed with Ala-Ala-Pro-Phe-Boronate (SEQ ID NO: 56) (Figure 7) in combination with sequence alignments of subtilisin BPN', KEX2, Furin, PC2, and P (Table 3) in designing basic specificity into the S1 and S2 and S4 subsites. The two subtilisin BPN' residues that most prominently display their side chains into the S4 pocket are Y104 and I107 (Figure 7).

Sequence alignments of subtilisin BPN' and the mammalian prohormone-processing proteases (Siezen, R. J., de Vos, W. M., Leunissen, A. M., and Dijkstra, B. W. (1991) *Prot. Eng.* 4:719-737) (Table 3) reveal that position 104 is conserved as Asp, and 107 as Glu in the prohormone converting (Arg-P4 specific) enzymes. Therefore these two mutations were introduced either individually or in combination into the dibasic-specific N62D/G166D subtilisin BPN' background (Table 4).

Table 3 Sequence alignments for the S4 site of subtilisins

S4 Site 100-110			
5	Subtilisin	GSGQYSWIING	(SEQ ID NO: 77)
	KEX2	GDITTEDEAAS	(SEQ ID NO: 78)
	Furin	GEVTDAVEARS	(SEQ ID NO: 79)
	PC2	PFMTDIIRASS	(SEQ ID NO: 80)
	P	GIVTDAIRASS	(SEQ ID NO: 81)

10 Table 4 describes oligonucleotides used for site-directed mutagenesis, protein regions affected by the mutations, and relative expression of protein for N62D/G166D subtilisin BPN' variants. Bold type indicates base changes from the pSS5 (N62D/G166D) template. For "Protein Expressed," "+" indicates a high level of expression of mature enzyme in crude culture medium, and "-" indicates no enzyme detectable.

TABLE 4

15	Mutant	Oligonucleotide	Protein Region	Pro- tein Ex- pres sed
	Y104D	5'- GGTTCGGCCAA.GATAGCTGGATCATT -3' (SEQ ID NO: 82)	S4 pocket	-
	I107E	5'- CCAATACAGCTGGGAAATTAACGGAATCG -3' (SEQ ID NO: 83)	S4 pocket	-
	Y104D/I107E	5'- GGTTCGGCCAAAGATAGCTGGGAAATTAACG GAATCGA -3' (SEQ ID NO: 84)	S4 pocket	-
20	A(-4)R/ A(-2)K/ Y(-1)R	5'- AAGAAGATCACGTAAGACATAAGCGCGCGC AGTCCGTGC -3' (SEQ ID NO: 85)	Proces- sing site	-
25	Y104D/ A(-4)R/ A(-2)K/ Y(-1)R	See individual mutations	S4 pocket + Proces- sing site	+
	I107E/ A(-4)R/ A(-2)K/ Y(-1)R	See individual mutations	S4 pocket + Proces- sing site	-
30	Y104D/I107E/ A(-4)R/ A(-2)K/ Y(-1)R	See individual mutations	S4 pocket + Proces- sing site	-

Initial attempts to express the triple mutants in *Bacillus* were unsuccessful, as indicated by SDS-PAGE of crude supernatants. We reasoned that the source of the expression problem could lie in the fact that correct folding and maturation of subtilisin requires autolytic cleavage of its propeptide (Power, S.D., Adams, R. M., and Wells, J. A. (1986) *Proc. Natl. Acad. Sci. USA* 83, 3096-3100). The processing site in the wild-type enzyme has a sequence that is optimized for the natural substrate preference, AHAYIA (1 denotes the site of cleavage). Although the N62D/G166D subtilisin can still autolyze itself with the wild-type processing site, the additional S4 pocket mutations could reduce the cleavage to the point where expression was lowered to a minute level.

To test whether the mutants were expressed poorly due to an inability to autolytically process itself, mutations in the processing site were simultaneously incorporated to accommodate the changes in substrate specificity. Thus the sequence from positions -4 to -1 was changed from AHAY to RHKR in combination with the S4 site mutations. For N62D/Y104D/G166D, high levels of expression could then be achieved providing an indication that the additional Y104D mutation induced an especially strong preference for P4 Arg over Ala. Variants containing the I107E mutation, however, could not be expressed even with the change in the processing site.

Kinetic analysis of variant subtilisins

The mature N62D/Y104D/G166D variant was purified and analyzed for its ability to hydrolyze several tetrapeptide-pNA substrates. Table 5 displays the results along with data for the N62D/G166D mutant and wild-type subtilisin.

Table 5

Kinetic analysis of WT, N62D/G166D, and N62D/Y104D/G166D subtilisin BPN' mutants versus succinyl-tetrapeptide-pNA substrates. Kinetic constants were determined from plots of initial rates versus substrate concentration. Units are as follows: k_{cat} , s^{-1} ; K_m , μM ; and k_{cat}/K_m , $M^{-1}s^{-1}$. Standard errors were less than 15%.

Tetrapeptide Sequence, P4-P3-P2-P1												
	AAPF			AAKR			RAKR			KAQR		
	k_{cat}	K_m	k_{cat}/K_m	k_{cat}	K_m	k_{cat}/K_m	k_{cat}	K_m	k_{cat}/K_m	k_{cat}	K_m	k_{cat}/K_m
Mutant												
WT	29	110	2.6×10^5	2.8	1700	1.7×10^{3a}	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.
N62D/ G166D	3.4	180	1.9×10^3	15	41	3.7×10^5	N.D. ^b	N.D. ^b	N.D. ^b	N.D.	N.D.	N.D.
N62D/ Y104D/ G166D	-	-	8.0×10^{0c}	0.27	34	8.1×10^3	11	23	4.9×10^5	9.8	29	3.4×10^5

^a Artificially low k_{cat}/K_m presumably due to competing cleavage between Lys and Arg

^b Biphasic reaction progress curves presumably due to multiple cleavages in the substrate

^c Unable to saturate the enzyme, apparent k_{cat}/K_m calculated from rates at low substrate concentrations assuming

$$v = (k_{cat}/K_m) (E) (S)$$

The tribasic substrates succinyl-RAKR-pNA (SEQ ID NO: 86) and succinyl-KAKR-pNA (SEQ ID NO: 87) were hydrolyzed with high catalytic efficiency (k_{cat}/K_m) by the triple mutant, at a level similar to wild-type subtilisin versus one of its best substrates, succinyl-AAPF-pNA (SEQ ID NO: 56). In contrast, the dibasic substrate succinyl-AAKR-pNA (SEQ ID NO: 67) was hydrolyzed 60-fold less efficiently, mostly
 5 due to diminution of k_{cat} . This indicates a dramatic specificity change from the wild-type preference at P4, at which hydrophobic residues are strongly favored over charged side chains (Grøn, H. and Breddam, K. (1992) *Biochemistry* 31, 8967-8971). In fact N62D/G166D subtilisin appears to cleave at an alternate site in the succinyl-RAKR-pNA (SEQ ID NO: 86) substrate, indicating that Arg was not accepted in its wild-type S4 site.

10 The large magnitude of the combined specificity changes in the N62D/Y104D/G166D variant is evidenced by its strong discrimination against substrates that are preferred by the wild-type enzyme. For example, succinyl-AAPF-pNA (SEQ ID NO: 56) is hydrolyzed 6×10^4 -fold less efficiently than succinyl-RAKR-pNA (SEQ ID NO: 86). Clearly, the S4 site mutation greatly improves upon the discriminatory power of the parent dibasic-specific N62D/G166D subtilisin, where the ratio of catalytic efficiency for
 15 succinyl-AAKR-pNA versus succinyl-AAPF-pNA is 1.9×10^2 . The improvement in discrimination (310-fold) is also higher than would be predicted from the data for hydrolysis of succinyl-RAKR-pNA (SEQ ID NO: 86) versus succinyl-AAKR-pNA (SEQ ID NO: 67) by the triple mutant (a 60-fold effect).

Therefore in order to produce subtilisin variants capable of cleaving substrates containing basic residues at positions P4, P2, and P1, additional site specific substitutions are made in the dibasic specific
 20 subtilisin variants. According to this aspect of the invention, substitution of the amino acid corresponding to Y104 of subtilisin BPN' produced by *Bacillus Amyloliquefaciens*, i.e., amino acid 104 of subtilisin BPN' or its equivalent, produces a variant having substantially altered substrate specificity. In a preferred embodiment of the present invention amino acids corresponding to N62, Y104, and G166 of subtilisin BPN' are substituted with acidic amino acids, preferably Asp and Glu and most preferably Asp. Subtilisin BPN'
 25 variants N62D/Y104D/G166D, N62D/Y104E/G166D, N62E/Y104D/G166E, N62E/Y104E/G166E, N62E/Y104D/G166D, N62E/Y104E/G166D, N62D/Y104E/G166E, and N62D/Y104D/G166E, and there equivalents are preferred. Most preferred among this group of subtilisin variants are the N62D/Y104D/G166D subtilisin BPN' variants and their equivalents.

Mutagenesis and Synthetic Techniques

30 Various techniques are available which may be employed to produce mutant DNA, which can encode the subtilisin variants of the present invention. For instance, it is possible to derive mutant DNA based on naturally occurring DNA sequences that encode for changes in an amino acid sequence of the resultant protein relative to a precursor subtilisin. These mutant DNA can be used to obtain the variants of the present invention.

35 According to the invention, specific residues of *B. amyloliquefaciens* subtilisin are identified for substitution. These amino acid residue position numbers refer to those assigned to the *B. amyloliquefaciens* subtilisin sequence (see the mature sequence in Fig. 1. of U.S. Patent No. 4,760,025). The invention, however, is not limited to the mutation of this particular subtilisin but extends to precursor subtilisins

containing amino acid residues which are equivalent, as defined herein, to the particular identified residues in *B. amyloliquefaciens* subtilisin. Equivalent amino acids can be found in, for instance, subtilisin Carlsberg from *Bacillus licheniformis*, Bode et al., (1986) EMBO J., 5:813-818; thermitase from *Thermoactinomyces vulgaris*, Gros et al., (1989) J. Mol. Biol. 210:347-367; and proteinase K from *Tritirachium album*, Betzel, et al., (1988) Acta Crystallogr., B, 44:163-172 as described by Siezen et al., (1991) Proc. Eng., 4: 719-737).

By way of illustration, with expression vectors encoding the precursor subtilisin in hand (see for example U.S. Patent No 4,760,025) site specific mutagenesis (Kunkel et al., (1991) Methods Enzymol. 204:125-139; Carter, P., et al., (1986) Nucl. Acids. Res. 13:4331; Zoller, M. J. et al., (1982) Nucl. Acids Res. 10:6487), cassette mutagenesis (Wells, J. A., et al., (1985) Gene 34:315), restriction selection mutagenesis (Wells, J. A., et al., (1986) Philos. Trans. R. Soc. London Ser A 317, 415) or other known techniques may be performed on the DNA. The mutant DNA can then be used in place of the parent DNA by insertion into the appropriate expression vectors. Growth of host bacteria containing the expression vectors with the mutant DNA allows the production of variants which can be isolated as described herein.

Oligonucleotide-mediated mutagenesis is a preferred method for preparing the variants of the present invention. This technique is well known in the art as described by Adelman et al., (1983) DNA, 2:183. Briefly, the native or unaltered DNA of a precursor subtilisin, for instance subtilisin BPN', is altered by hybridizing an oligonucleotide encoding the desired mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the precursor.

After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the DNA.

Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as those described by Crea et al. (1987) Proc. Natl. Acad. Sci. USA, 75:5765. Exemplary oligonucleotide sequences for introducing amino acid changes into precursor subtilisin BPN' are provided in Tables 2 and 4.

Single-stranded DNA template may also be generated by denaturing double-stranded plasmid (or other) DNA using standard techniques.

For alteration of the native DNA sequence (to generate amino acid sequence variants, for example), the oligonucleotide is hybridized to the single-stranded template under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of DNA polymerase I, is then added to synthesize the complementary strand of the template using the oligonucleotide as a primer for synthesis. A heteroduplex molecule is thus formed such that one strand of DNA encodes the variant form of the subtilisin, and the other strand (the original template) encodes the native, unaltered sequence of the precursor subtilisin. This heteroduplex molecule is then transformed into a suitable host cell. After the cells are grown, they are plated onto agarose plates and screened using the oligonucleotide primer radiolabeled with 32-phosphate to

identify the bacterial colonies that contain the mutated DNA. The mutated region is then removed and placed in an appropriate vector for protein production, generally an expression vector of the type typically employed for transformation of an appropriate host.

The method described immediately above may be modified such that a homoduplex molecule is created wherein both strands of the plasmid contain the mutation(s). The modifications are as follows: The single-stranded oligonucleotide is annealed to the single-stranded template as described above. A mixture of three deoxyribonucleotides, deoxyriboadenosine (dATP), deoxyriboguanosine (dGTP), and deoxyribothymidine (dTTP), is combined with a modified thio-deoxyribocytosine called dCTP-(α S) (which can be obtained from Amersham Corporation). This mixture is added to the template-oligonucleotide complex. Upon addition of DNA polymerase to this mixture, a strand of DNA identical to the template except for the mutated bases is generated. In addition, this new strand of DNA will contain dCTP-(α S) instead of dCTP, which serves to protect it from restriction endonuclease digestion.

After the template strand of the double-stranded heteroduplex is nicked with an appropriate restriction enzyme, the template strand can be digested with ExoIII nuclease or another appropriate nuclease past the region that contains the site(s) to be mutagenized. The reaction is then stopped to leave a molecule that is only partially single-stranded. A complete double-stranded DNA homoduplex is then formed using DNA polymerase in the presence of all four deoxyribonucleotide triphosphates, ATP, and DNA ligase. This homoduplex molecule can then be transformed into a suitable host cell as described above.

DNA encoding variants with more than one amino acid to be substituted may be generated in one of several ways. If the amino acids are located close together in the polypeptide chain, they may be mutated simultaneously using one oligonucleotide that codes for all of the desired amino acid substitutions. If, however, the amino acids are located some distance from each other (separated by more than about ten amino acids), it is more difficult to generate a single oligonucleotide that encodes all of the desired changes. Instead, one of two alternative methods may be employed.

In the first method, a separate oligonucleotide is generated for each amino acid to be substituted. The oligonucleotides are then annealed to the single-stranded template DNA simultaneously, and the second strand of DNA that is synthesized from the template will encode all of the desired amino acid substitutions.

The alternative method involves two or more rounds of mutagenesis to produce the desired mutant. The first round is as described for the single mutants: wild-type DNA is used for the template, an oligonucleotide encoding the first desired amino acid substitution(s) is annealed to this template, and the heteroduplex DNA molecule is then generated. The second round of mutagenesis utilizes the mutated DNA produced in the first round of mutagenesis as the template. Thus, this template already contains one or more mutations. The oligonucleotide encoding the additional desired amino acid substitution(s) is then annealed to this template, and the resulting strand of DNA now encodes mutations from both the first and second rounds of mutagenesis. This resultant DNA can be used as a template in a third round of mutagenesis, and so on.

Cleavage of a Fusion Proteins With Subtilisin Variants

A fusion protein is any polypeptide that contains within it an affinity domain (AD) that usually aids in protein purification, a protease cleavage sequence or substrate linker (SL), which is cleaved by a protease and a protein product of interest (PP). Such fusion proteins are generally expressed by recombinant DNA technology. The genes for fusion proteins are designed so that the SL is between the AD and PP. These usually take the form AD-SL-PP such that the domain closest to the N-terminus is AD and PP is closest to the C-terminus.

Examples of AD would include, glutathione-S-transferase which binds to glutathione, protein A (or derivatives or fragments thereof) which binds IgG molecules, poly-histidine sequences, particularly (His)₆ (SEQ ID NO: 51) that bind metal affinity columns, maltose binding protein that binds maltose, human growth hormone that binds the human growth hormone receptor or any of a variety of other proteins or protein domains that can bind to an immobilized affinity support with an association constant (K_a) of $>10^5$ M⁻¹.

The SL can be any sequence which is cleaved by the subtilisin variants of the present invention. In preparations where the variant N62D/Y104D/G166D or its equivalent are used the SL can be any sequence, preferably at least 4 amino acids, in which the P₄, P₂, and P₁ residues are basic residues. Therefore a SL linker is employed of the general formula P₄-P₃-P₂-P₁ wherein P₄, P₂, and P₁ are basic amino acid residues. Preferred SLs according to this aspect of the invention include Lys-Ala-Lys-Arg (SEQ ID NO: 87) and Arg-Ala-Lys-Arg (SEQ ID NO: 86).

Likewise, where the N62D/G166D subtilisin variant is contemplated the SL preferably contains dibasic residues. For the variants capable of cleaving substrates containing dibasic residues the SL should be at least four residues and preferably contain a large hydrophobic residue at P₄ (such as Leu or Met) and dibasic residues at P₂ and P₁ (such as Arg and Lys). A particularly good substrate is Leu-Met-Arg-Lys (SEQ ID NO: 52), but a variety of other sequences may work including Ala-Ser-Arg-Arg (SEQ ID NO: 50) and even Leu-Thr-Ala-Arg (SEQ ID NO 53).

It is often useful that the SL contain a flexible segment on its N-terminus to better separate it from the AD and PP. Such sequences include Gly-Pro-Gly-Gly (SEQ ID NO: 54) but can be as simple as Gly-Gly or Pro-Gly. Thus, an example of a particularly good SL would have the sequence Gly-Pro-Gly-Gly-Leu-Met-Arg-Lys (SEQ ID NO: 88) in the case of subtilisin variants capable of cleaving substrates containing dibasic amino acids, or Gly-Pro-Gly-Gly-Lys-Ala-Lys-Arg (SEQ ID NO: 89). This sequence would be inserted between the AD and PP domains.

The PP can be virtually any protein or peptide of interest but preferably should not have a Pro, Ile, Thr, Val, Asp or Glu as its first residue (P₁'), or Pro or Gly at the second residue (P₂') or Pro at the third residue (P₃'). Such residues are poor substrates for the enzyme and may impair the ability of the subtilisins variant to cleave the SL sequence.

The conditions for cleaving the fusion protein are best done in aqueous solution, although it should be possible to immobilize the enzyme and cleave the soluble fusion protein. It may also be possible to cleave the fusion protein as it remains immobilized on a solid support (e.g. bound to the solid support through AD) with the soluble subtilisin variant. It is preferable to add the enzyme to the fusion protein so that the enzyme

is less than one part in 100 (1:100) by weight. A good buffer is 10-50mM Tris (pH 8.2) in 10mM NaCl. A preferable temperature is about 25°C although the enzyme is active up to 65°C. The extent of cleavage can be assayed by applying samples to SDS-PAGE. Generally suitable conditions for using the subtilisin variants of this invention do not depart substantially from those known in the art for the use of other subtilisins.

EXAMPLES

In the examples below and elsewhere, the following abbreviations are employed: subtilisin BPN', subtilisin from *Bacillus amyloliquefaciens*; Boc-RVRR-MCA (SEQ ID NO. 73), N-t-butoxy carbonyl-arginine-valine-arginine-arginine-7-amido-4-methyl coumarin; suc-Ala-Ala-Pro-Phe-pna (SEQ ID NO. 56), N-succinyl-alanine-alanine-proline-phenylalanyl-p-nitroanalide (SEQ ID NO. 56); hGH, human growth hormone; hGHbp, extracellular domain of the hGH receptor; PBS, phosphate buffered saline; AP, alkaline phosphatase;

Example 1

Construction and Purification of Subtilisin Mutants.

Site-directed mutations were introduced into the subtilisin BPN' gene cloned into the phagemid pSS5 (Wells, J. A., Ferrari, E., Henner, D. J., Estell, D.A. and Chen, E. Y. (1983) *Nucl. Acids Res.* 11:7911-7929). Single-stranded uracil-containing pSS5 template was prepared and mutagenesis performed using the method of Kunkel (Kunkel, T. A., Bebenek, K and McClary, J. (1991) *Methods Enzymol.* 204:125-139). For example, the synthetic oligonucleotide N62D,

(5'- CCAAGACAACG*ACTCTCACGGAA -3') (SEQ ID NO. 25)

in which the asterisk denotes a mismatch to the wild-type sequence, was used to construct the N62D mutant. The oligonucleotide was first phosphorylated at the 5' end using T4 polynucleotide kinase according to a described procedure (Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) in "Molecular Cloning: A Laboratory Manual," Second Edition, Cold Spring Harbor, N.Y.). The phosphorylated oligonucleotide was annealed to single-stranded uracil-containing pSS5 template, the complementary DNA strand was filled in with deoxynucleotides using T7 polynucleotide kinase, and the resulting nicks ligated using T4 DNA ligase according to a previously described procedure (Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) in "Molecular Cloning: A Laboratory Manual," Second Edition, Cold Spring Harbor, N.Y.). Heteroduplex DNA was transformed into the E. coli host JM101 (Yanish-Perron, C., Viera, J., and Messing, J. (1985) *Gene* 33: 103-199), and putative mutants were confirmed by preparation and dideoxy nucleotide sequencing of single stranded DNA (Sanger, F., Nicklen, S. and Coulson, A. R. (1977) *Proc. Natl. Acad. Sci. USA* 74:5463-5467) according to the SEQUENASE® protocol (USB Biochemicals). Mutant single-stranded DNA was then retransformed into JM101 cells and double stranded DNA prepared according to a previously

described procedure (Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) in "Molecular Cloning: A Laboratory Manual," Second Edition, Cold Spring Harbor, N.Y.). For other mutations also requiring the use of one primer, the oligonucleotides used are listed in Table 2. For several of these oligonucleotides, additional silent mutations emplacing new restriction sites were simultaneously introduced to provide an
5 alternative verification of mutagenesis.

To construct the double mutants N62D/G166D, and N62D/G166E, pSS5 DNA containing the N62D mutation was produced in single-stranded uracil-containing form using the Kunkel procedure (Kunkel, T. A., Bebenek, K and McClary, J. (1991) *Methods Enzymol.* 204, 125-139). This mutant DNA was used as template for the further introduction of the G166D or G166E mutations, using the appropriate
10 oligonucleotide primers (see sequences in Table 2), following the procedures described above.

To construct the triple mutants, such as N62D/Y104D/G166D, pSS5 DNA containing the N62D/G166D mutation or other appropriate double mutation, was produced in single-stranded uracil-containing form using the Kunkel procedure (Kunkel, T. A., Bebenek, K and McClary, J. (1991) *Methods Enzymol.* 204, 125-139). This mutant DNA was used as template for the further introduction of the Y104D
15 mutations, using the appropriate oligonucleotide primers (see sequences in Table 4), following the procedures described above.

For expression of the subtilisin BPN' mutants, double stranded mutant DNA was transformed into a protease-deficient strain (BG2036) of *Bacillus Subtilis* (Yang, M. Y., Ferrari, E. and Henner, D. J. (1984) *Journal of Bacteriology* 160:15-21) according to a previous method (Anagnostopoulous, C. and
20 Spizizen, J. (1961) *Journal of Bacteriology* 81:741-746) in which transformation mixtures were plated out on LB plus skim milk plates containing 12.5 µg/mL chloramphenicol. The clear halos indicative of skim milk digestion surrounding transformed colonies were noted to roughly estimate secreted protease activity.

The transformed BG2036 strains were cultured by inoculating 5 mL of 2xYT media (Miller, J. H., (1972) in "Experiments in Molecular Genetics," Cold Spring Harbor, N.Y.) containing 12.5 µg/mL
25 chloramphenicol and 2 mM CaCl₂ at 37 °C for 18-20 h, followed by 1:100 dilution in the same medium and growth in shake flasks at 37 °C for 18-22 h with vigorous aeration. The cells were harvested by centrifugation (6000g, 15 min, 4°C), and to the supernatant 20mM (final) CaCl₂ and one volume of ethanol (-20°C) were added. After 30 min at 4°C, the solution was centrifuged (12,000g, 15 min, 4°C), and one volume of ethanol (-20°C) added to the supernatant. After 2 h at -20°C, the solution was centrifuged
30 (12,000g, 15 min, 4°C) and the pellet resuspended in and dialyzed against MC (25 mM 2-(N-Morpholino)ethanesulfonic acid (MES), 5 mM CaCl₂ at pH 5.5) overnight at 4°C. The dialysate was passed through a 0.22 µm syringe filter and loaded onto a mono-S cation exchange column run by an FPLC system (Pharmacia Biotechnology). The column was washed with 20 volumes of MC and mutant subtilisin eluted over a linear gradient of zero to 0.15 M NaCl in MC, all at a flow rate of 1 mL/min. Peak fractions were
35 recovered and the subtilisin mutant quantitated by measuring the absorbance at 280 nm ($E_{280} 0.1\% = 1.17$) (Matsubara, H.; Kasper, C B.; Brown, D. M.; and Smith, E. L. (1965) *J. Biol. Chem.*, 240:1125-1130.)

Example 2

Kinetic Characterizations

Subtilisins were assayed by measuring the initial rates of hydrolysis of *p*-nitroanilide tetrapeptide substrates in 0.4 mL 20 mM Tris-Cl pH 8.2, 4 % (v/v) dimethyl sulfoxide at (25 ± 0.2)°C as described previously (Estell, D. A., Graycar, T. P., Miller, J. V., Powers, D. B., Burnier, J. P., Ng, P. G. and Wells, J. A. (1986)*Science* 233:659-663). Enzyme concentrations (E)₀ were determined spectrophotometrically using E_{280 nm} 0.1% = 1.17 (Matsubara, H.; Kasper, C B.; Brown, D. M.; and Smith, E. L. (1965)*J. Biol. Chem.*, 240:1125-1130.), and were typically 5-50 nM in reactions. Initial rates were determined for nine to twelve different substrate concentrations over the range of 0.001-2.0 mM. Plots of initial rates (v) versus substrate concentration (S) were fitted to the Michaelis-Menton equation,

$$v = \frac{k_{cat}(E)_0((S))}{K_m + (S)}$$

to determine the kinetic constants k_{cat} and K_m (Fersht, A. in "Enzyme Structure and Mechanism", Second edition, Freeman and Co., N.Y.) using the program Kaleidagraph (Synergy Software, Reading, PA).

Example 3

Substrate Phage

Substrate phage selections were performed as described by Matthews and Wells (Matthews, D. J. and Wells, J. A. (1993)*Science* 260:1113-1117), with minor modifications. Phage sorting was carried out using a library in which the linker sequence between the gene III coat protein and a tight-binding variant of hGH was GPGGX₃GGPG (SEQ ID NO. 52). The library contained 2 x 10⁶ independent transformants. Phage particles were prepared by infecting 1 mL of log phase 27C7 (F/tet^R/Omp^R/degP^R) *Escherichia coli* with approximately 10⁸ library phage for 1 h at 37°C, followed by 18-24 h of growth in 25 mL 2YT medium containing 10¹⁰ M13K07 helper phage and 50 µg/mL carbenicillin at 37°C. Wells of a 96-well Nunc Maxisorb microtiter plate were coated with 2 µg/mL of hGHbp in 50 mM NaHCO₃ at pH 9.6 overnight at 4°C and blocked with PBS (10 mM sodium phosphate at pH 7.4 and 150 mM NaCl) containing 2.5% (w/v) skim milk for 1 h at room temperature. Between 10¹¹ and 10¹² phage in 0.1 mL 10 mM tris-Cl (pH 7.6), 1 mM EDTA, and 100 mM NaCl were incubated in the wells at room temperature for 2 h with gentle agitation. The plate was washed first with 20 rinses of PBS plus 0.05% Tween 20 and then twice with 20 mM tris-Cl at pH 8.2. The N62D/G166D subtilisin was added in 0.1 mL of 20 mM tris-Cl at pH 8.2 and protease sensitive phage were eluted after a variable reaction time. The concentration of protease and incubation times for elution of sensitive phage were decreased gradually over the course of sorting procedure to increase selectivity, with protease concentrations of 0.2 nM (rounds 1-3) and 0.1 nM (rounds 4-9), and reaction times of 5 min (rounds 1-6), 2.5 min (round 7), 40 s (round 8) and 20 s (round 9). Control wells in which no protease was added were also included in each round. For the resistant phage pool, the incubation time with protease remained constant at 5 min. The wells were then washed ten times with PBS plus 0.05% Tween 20 and resistant phage eluted by treatment with 0.1 mL of 0.2 M glycine at pH 2.0 in PBS plus 0.05% Tween

20 for 1 min at room temperature. Protease sensitive and resistant phage pools were titred and used to infect log phase 27C7 cells for 1 h at 37°C, followed by centrifugation at 4000 rpm, removal of supernatant, and resuspension in 1 mL 2YT medium. The infected cells were then grown 18-24 h in the presence of helper phage as described above and the process repeated 9 times. Selected substrates were introduced into
5 AP fusion proteins and assayed for relative rates of cleavage as described by Matthews and Wells (Matthews, D. J., Goodman, L. J., Gorman, C. M., and Wells, J. A. (1994) *Protein Science* 3:1197-1205 and Matthews, D. J. and Wells, J. A. (1993) *Science* 260:1113-1117), except that the cleavage reactions were performed in 20 mM Tris-Cl at pH 8.2.

Example 4

10 *Substrate phage selection and cleavage of a fusion protein*

Subtilisin has the capability to bind substrates from the P4 to P3' positions (McPhalen, C. A. and James, N. G. (1988) *Biochemistry* 27:6582-6598 and Bode, W., Papamokos, E., Musil, D., Seemueller, U. and Fritz, M. (1986) *EMBO J.* 5:813-818). Given this extensive binding site and the apparent cooperative nature in the way the substrate can bind the enzyme we wished to explore more broadly the substrate
15 preferences for the enzyme. To do this we utilized the substrate phage selection (Matthews, D. J., Goodman, L. J., Gorman, C. M., and Wells, J. A. (1994) *Protein Science* 3:1197-1205 and Matthews, D. J. and Wells, J. A. (1993) *Science* 260:1113-1117) described in Example 3. In this method a five-residue substrate linker that was flanked by di-glycine residues is inserted between an affinity domain (in this case a high affinity variant of hGH) and the carboxy-terminal domain of gene III, a minor coat protein displayed on the surface
20 of the filamentous phage, M13. The five residue substrate linker is fully randomized to generate a library of 20⁵ different protein sequence variants. These are displayed on the phage particles which are allowed to bind to the hGHbp. The protease of interest was added and if it cleaved the phage particle at the substrate linker it released that particle. The particles released by protease treatment can be propagated and subjected to another round of selection to further enrich for good protease substrates. Sequences that are retained can
25 also be propagated to enrich for poor protease substrates. By sequencing the isolated phage genes at the end of either selection one can identify good and poor substrates for further analysis.

We chose to focus on the subtilisin BPN' variant N62D/G166D as it was slightly better at discriminating the synthetic dibasic substrates from the others. We subjected the substrate phage library to nine rounds of selection with the subtilisin variant and isolated clones that were either increasingly sensitive
30 or resistant to cleavage. Of twenty-one clones sequenced from the sensitive pool eighteen contained dibasic residues, eleven of which had the substrate linker sequence Asn-Leu-Met-Arg-Lys (SEQ ID NO: 35) (Table 6).

TABLE 6

Substrate phage sequences sensitive or resistant to N62D/G166D subtilisin from a GG-xxxxx-GG library after 9 rounds of selection^a.

Protease Sensitive Pool

5	<u>No Basic Sites (0)</u>	<u>Monobasic Sites (3)</u>	<u>Dibasic Sites (18)</u>
		N L T A R (3) (SEQ ID NO: 34)	N L M R K (11) (SEQ ID NO: 35)
			T A S R R (4) (SEQ ID NO: 36)
			L T R R S (SEQ ID NO: 37)
			A L S R K (SEQ ID NO: 38)
			L M L R K (SEQ ID NO: 39)

Protease Resistant Pool

	<u>No Basic Sites (7)</u>	<u>Monobasic Sites (2)</u>	<u>Dibasic Sites (1)</u>
	A S T H F (SEQ ID NO: 40)	Q K P N F (SEQ ID NO: 41)	R K P T H (SEQ ID NO: 42)
10	I Q Q Q Y (SEQ ID NO: 43)	R P G A M (SEQ ID NO: 44)	
	Q G E L P (SEQ ID NO: 47)		
15	A P D P T (SEQ ID NO: 46)		
	Q L L E H (SEQ ID NO: 47)		
	V N N N H (SEQ ID NO: 48)		
20	A Q S N L (SEQ ID NO: 49)		

^a Numbers in parentheses indicate the number of times a particular DNA sequence was isolated.

Three (3) of the sensitive sequences were monobasic, Asn-Leu-Thr-Ala-Arg (SEQ ID NO: 34). It is known that subtilisin has a preference for hydrophobic residues at the P4 position. If these and the other
 25 selected substrates were indeed cleaved after the last basic residue they all would have a Leu, Met or Ala at the P4 position. Almost no basic residues were isolated in the protease resistant pool and those that were had a Pro following the mono- or dibasic residue. It is known that subtilisin does not cleave substrates containing

Pro at the P1' position (Carter, P., Nilsson, B., Burnier, J., Burdick, D. and Wells, J. A. (1989) *Proteins: Struct., Funct., Genet.* 6:240-248). Thus, di-basic substrates were highly selected and these had the additional feature of Leu, Met or Ala at the P4 position.

Example 5

Cleavage of Substrate Linkers

5 We wished to analyze how efficiently the most frequently selected sequences were cleaved in the context of a fusion protein. For this we applied an alkaline phosphatase-fusion protein assay (Matthews, D. J., Goodman, L. J., Gorman, C. M., and Wells, J. A. (1994)*Protein Science* 3:1197-1205 and Matthews, D. J. and Wells, J. A. (1993)*Science* 260:1113-1117). The hGH substrate linker domains were excised from the
10 phage vector by PCR and fused in front of the gene for *E. coli* AP. The fusion protein was expressed and purified on an hGH receptor affinity column. The fusion protein was bound to the hGH receptor on a plate and treated with the subtilisin variant. The rate of cleavage of the fusion protein from the plate was monitored by collecting soluble fractions as a function of time and assaying for AP activity (Figure 5). The most
15 frequently isolated substrate sequence, Asn-Leu-Met-Arg-Lys (SEQ ID NO: 35) was cleaved about ten times faster than the next most frequently isolated clones (Thr-Ala-Ser-Arg-Arg (SEQ ID NO: 36) and Asn-Leu-Thr-Ala-Arg (SEQ ID NO: 34). The cleaved AP products were also recovered and subjected to N-terminal sequencing to determine the sites of cleavage (Figure 5), cleavage site denoted by †). In all three fusion proteins, this site was immediately following the dibasic or monobasic site according to the mutant subtilisin design. We also tested the dibasic sequence isolated from the resistant pool, namely Arg-Lys-Pro-Thr-His
20 (SEQ ID NO: 42). We observed no detectable cleavage above background for this substrate during the assay.

25 The present invention has of necessity been discussed herein by reference to certain specific methods and materials. It is to be understood that the discussion of these specific methods and materials in no way constitutes any limitation on the scope of the present invention, which extends to any and all alternative materials and methods suitable for accomplishing the ends of the present invention.

• • • • •

All references cited herein are expressly incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Genentech, Inc.
- (ii) TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
SUBSTRATES CONTAINING BASIC RESIDUES
- (iii) NUMBER OF SEQUENCES: 89
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/398028
(B) FILING DATE: 03-MAR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kubinec, Jeffrey S.
(B) REGISTRATION NUMBER: 36,575
(C) REFERENCE/DOCKET NUMBER: P0936P1PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-8228
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8119 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCNGGT CTAATAAAAT ATTATTCCAT ACTATACAAT TAATACACAG 50

AATAATCTGT CTATTGGTTA TTCTGCAAAT GAAAAAAGG AGAGGATAAA 100

GA GTG AGA GGC AAA AAA GTA TGG ATC AGT TTG CTG TTT 138
Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe
-107 -105 -100

GCT TTA GCG TTA ATC TTT ACG ATG GCG TTC GGC AGC ACA 177
Ala Leu Ala Leu Ile Phe Thr Met Ala Phe Gly Ser Thr

	-95		-90		-85	
	TCC TCT GCC CAG GCG GCA GGG AAA TCA AAC GGG GAA AAG 216					
	Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys					
	-80		-75		-70	
5	AAA TAT ATT GTC GGG TTT AAA CAG ACA ATG AGC ACG ATG 255					
	Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met					
	-65		-60			
	AGC GCC GCT AAG AAG AAA GAT GTC ATT TCT GAA AAA GGC 294					
	Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly					
10	-55		-50		-45	
	GGG AAA GTG CAA AAG CAA TTC AAA TAT GTA GAC GCA GCT 333					
	Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala					
	-40		-35			
	TCA GCT ACA TTA AAC GAA AAA GCT GTA AAA GAA TTG AAA 372					
15	Ser Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys					
	-30		-25		-20	
	AAA GAC CCG AGC GTC GCT TAC GTT GAA GAA GAT CAC GTA 411					
	Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Val					
	-15		-10		-5	
20	GCA CAT GCG TAC GCG CAG TCC GTG CCT TAC GGC GTA TCA 450					
	Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser					
	1		5			
	CAA ATT AAA GCC CCT GCT CTG CAC TCT CAA GGC TAC ACT 489					
	Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr					
25	10		15		20	
	GGA TCA AAT GTT AAA GTA GCG GTT ATC GAC AGC GGT ATC 528					
	Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile					
	25		30		35	
	GAT TCT TCT CAT CCT GAT TTA AAG GTA GCA GGC GGA GCC 567					
	Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala					
30	40		45			
	AGC ATG GTT CCT TCT GAA ACA AAT CCT TTC CAA GAC AAC 606					
	Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn					
	50		55		60	
	GAC TCT CAC GGA ACT CAC GTT GCC GGC ACA GTT GCG GCT 645					
35	Asp Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala					
	65		70			
	CTT AAT AAC TCA ATC GGT GTA TTA GGC GTT GCG CCA AGC 684					
	Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser					
40	75		80		85	
	GCA TCA CTT TAC GCT GTA AAA GTT CTC GGT GCT GAC GGT 723					
	Ala Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly					
	90		95		100	
	TCC GGC CAA TAC AGC TGG ATC ATT AAC GGA ATC GAG TGG 762					
	Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp					
45	105		110			
	GCG ATC GCA AAC AAT ATG GAC GTT ATT AAC ATG AGC CTC 801					
	Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu					
	115		120		125	

GGC GGA CCT TCT GGT TCT GCT GCT TTA AAA GCG GCA GTT 840
 Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val
 130 135

5 GAT AAA GCC GTT GCA TCC GGC GTC GTA GTC GTT GCG GCA 879
 Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala
 140 145 150

GCC GGT AAC GAA GGC ACT TCC GGC AGC TCG TCG ACA GTG 918
 Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser Thr Val
 155 160 165

10 GAC TAC CCT GGC AAA TAC CCT TCT GTC ATT GCA GTA GGC 957
 Asp Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly
 170 175

GCT GTT GAC AGC AGC AAC CAA AGA GCA TCT TTC TCA AGC 996
 Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser
 180 185 190

15 GTA GGA CCT GAG CTT GAT GTC ATG GCA CCT GGC GTA TCT 1035
 Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser
 195 200

ATC CAA AGC ACG CTT CCT GGA AAC AAA TAC GGG GCG TAC 1074
 Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr
 205 210 215

AAC GGT ACC TCA ATG GCA TCT CCG CAC GTT GCC GGA GCG 1113
 Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala
 220 225 230

25 GCT GCT TTG ATT CTT TCT AAG CAC CCG AAC TGG ACA AAC 1152
 Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp Thr Asn
 235 240

ACT CAA GTC CGC AGC AGT TTA GAA AAC ACC ACT ACA AAA 1191
 Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
 245 250 255

30 CTT GGT GAT TCT TTC TAC TAT GGA AAA GGG CTG ATC AAC 1230
 Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn
 260 265

GTA CAG GCG GCA GCT CAG TA AAACATAAAA AACCGGCCTT 1270
 Val Gln Ala Ala Ala Gln
 270 275

GGCCCCGCCG GTTTTTTATT ATTTTCTTC CTCCGCATGT TCAATCCGCT 1320

CCATAATCGA CGGATGGCTC CCTCTGAAAA TTTTAACGAG AAACGGCGGG 1370

TTGACCCGGC TCAGTCCCGT AACGGCCAAG TCCTGAAACG TCTCAATCGC 1420

40 CGCTTCCCGG TTTCCGGTCA GCTCAATGCC GTAACGGTCG GCGGCGTTTT 1470

CCTGATACCG GGAGACGGCA TTCGTAATCG GATCCGGAAA TTGTAAACGT 1520

TAATATTTTG TTAAAATTCG CGTTAAATTT TTGTAAATC AGCTCATTTT 1570

TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC AAAAGAATAG 1620

ACCGAGATAG GGTGAGTGT TGTTCCAGTT TGAACAAGA GTCCACTATT 1670

45 AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCT 1720

ATGGCCCACT ACGTGAACCA TCACCCTAAT CAAGTTTTTT GGGGTCGAGG 1770
TGCCGTAAAG CACTAAATCG GAACCCTAAA GGGAGCCCC GATTTAGAGC 1820
TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA 1870
AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA 1920
5 ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG CGTCCGGATC 1970
NGATCCGACG CGAGGCTGGA TGGCCTTCCC CATTATGATT CTTCTCGCTT 2020
CCGGCGGCAT CGGGATGCCC GCGTTGCAGG CCATGCTGTC CAGGCAGGTA 2070
GATGACGACC ATCAGGGACA GCTTCAAGGA TCGCTCGCGG CTCTTACCAG 2120
CCTAACTTCG ATCACTGGAC CGCTGATCGT CACGGCGATT TATGCCGCCT 2170
10 CGGCGAGCAC ATGGAACGGG TTGGCATGGA TTGTAGGCGC CGCCCTATAC 2220
CTTGTCTGCC TCCCCGCGTT GCGTCGCGGT GCATGGAGCC GGGCCACCTC 2270
GACCTGAATG GAAGCCGGCG GCACCTCGCT AACGGATTCA CCACTCCAAG 2320
AATTGGAGCC AATCAATTCT TGCGGAGAAC TGTGAATGCG CAAACCAACC 2370
CTTGGCAGAA CATATCCATC GCGTCCGCCA TCTCCAGCAG CCGCACGCGG 2420
15 CGCATCTCGG GCCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCTG 2470
ACGAGCATCA CAAAATCGA CGCTCAAGTC AGAGGTGGCG AAACCCGACA 2520
GGACTATAAA GATACCAGGC GTTTCCCCCT GGAAGCTCCC TCGTGCCTC 2570
TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTTCTCCCTT 2620
CGGGAAGCGT GCGCTTTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTCG 2670
20 GTGTAGGTCG TTCGCTCCAA GCTGGGCTGT GTGCACGAAC CCCCCGTTCA 2720
GCCCAGCCGC TCGCCTTAT CCGGTAAC TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA CAGGATTAGC 2820
AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA 2870
CTACGGCTAC ACTAGAAGGA CAGTATTGAG TATCTGCGCT CTGCTGAAGC 2920
25 CAGTTACCTT CGGAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC 2970
ACCCTGGTA GCGGTGGTTT TTTGTTTGC AAGCAGCAGA TTACGCGCAG 3020
AAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTCTACG GGGTCTGACG 3070
CTCAGTGGA CGAAACTCA CGTTAAGGGA TTTTGGTCAT GAGATTATCA 3120
AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC 3170
30 AATCTAAAGT ATATATGAGT AAAGTTGGTC TGACAGTTAC CAATGCTTAA 3220
TCAGTGAGGC ACCTATCTCA GCGATCTGTC TATTTCGTTT ATCCATAGTT 3270
GCCTGACTCC CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC 3320
TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG 3370

ATTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT 3420
CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT GCCGGGAAGC 3470
TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG 3520
CTGCAGGCAT CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTACAGC 3570
5 TCCGGTTCCTC AACGATCAAG GCGAGTTACA TGATCCCCCA TGTGTGCAA 3620
AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG 3670
CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT 3720
GTCATGCCAT CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA 3770
GTCATTCTGA GAATAGTGTA TCGGGCGACC GAGTTGCTCT TGCCCGGCGT 3820
10 CAACACGGGA TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC 3870
ATTGGA AAC GTTCTTCGGG GCGAAACTC TCAAGGATCT TACCGCTGTT 3920
GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT 3970
CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG AAGGCAAAAT 4020
GCCGCAAAAA AGGGAATAAG GCGGACACGG AAATGTTGAA TACTCATACT 4070
15 CTTCCTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA 4120
GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT AGGGGTTCCG 4170
CGCACATTTT CCCGAAAAGT GCCACCTGAC GTCTAAGAAA CCATTATTAT 4220
CATGACATTA ACCTATAAAA ATAGGCGTAT CACGAGGCCC TTTCGTCTTC 4270
AAGAATTAAT TCCTTAAGGA ACGTACAGAC GGCTTAAAG CCTTTAAAAA 4320
20 CGTTTTTAAG GGGTTTGTAG ACAAGGTAAA GGATAAAACA GCACAATTCC 4370
AAGAAAAACA CGATTAGAA CCTAAAAGA ACGAATTGA ACTAACTCAT 4420
AACCAGAGAG TAAAAAAGA ACGAAGTCGA GATCAGGGAA TGAGTTTATA 4470
AAATAAAAAA AGCACCTGAA AAGGTGTCTT TTTTGTATGG TTTTGAACCT 4520
GTTCTTTCTT ATCTTGATAC ATATAGAAAT AACGTCATTT TTATTTTAGT 4570
25 TGCTGAAAGG TCGTTGAAG TGTGGTATG TATGTGTTTT AAAGTATTGA 4620
AAACCCTTAA AATTGGTTGC ACAGAAAAAC CCCATCTGTT AAAGTTATAA 4670
GTGACTAAAC AAATAACTAA ATAGATGGGG GTTCTTTTA ATATTATGTG 4720
TCCTAATAGT AGCATTTATT CAGATGAAAA ATCAAGGGTT TTAGTGGACA 4770
AGACAAAAAG TGGAAAAGTG AGACCATGGA GAGAAAAGAA AATCGCTAAT 4820
30 GTTGATTACT TTGAACTTCT GCATATTCTT GAATTTAAAA AGGCTGAAAG 4870
AGTAAAAGAT TGTGCTGAAA TATTAGAGTA TAAACAAAT CGTGAAACAG 4920
GCGAAAGAAA GTTGATCGA GTGTGGTTTT GTAAATCCAG GCTTTGTCCA 4970
ATGTGCAACT GGAGGAGAGC AATGAAACAT GGCATTTCAGT CACAAAAGGT 5020

TGTTGCTGAA GTTATTAAAC AAAAGCCAAC AGTTCGTTGG TTGTTTCTCA 5070
CATTAAACAGT TAAAAATGTT TATGATGGCG AAGAATTAAA TAAGAGTTTG 5120
TCAGATATGG CTCAAGGATT TCGCCGAATG ATGCAATATA AAAAAATTAA 5170
TAAAAATCTT GTTGGTTTTA TCGGTGCAAC GGAAGTGACA ATAAATAATA 5220
5 AAGATAATTC TTATAATCAG CACATGCATG TATTGGTATG TGTGGAACCA 5270
ACTTATTTTA AGAATACAGA AACTACGTG AATCAAAAAC AATGGATTCA 5320
ATTTTGAAA AAGGCAATGA AATTAGACTA TGATCCAAAT GTAAAAGTTC 5370
AAATGATTCG ACCGAAAAAT AAATATAAAT CGGATATACA ATCGGCAATT 5420
GACGAACTG CAAAATATCC TGTAAGGAT ACGGATTTTA TGACCGATGA 5470
10 TGAAGAAAAG AATTGAAAC GTTGTCTGA TTTGGAGGAA GGTTCACACC 5520
GTAAAAGGTT AATCTCCTAT GGTGGTTTGT TAAAAGAAAT ACATAAAAAA 5570
TTAAACCTTG ATGACACAGA AGAAGGCGAT TTGATTCATA CAGATGATGA 5620
CGAAAAAGCC GATGAAGATG GATTTTCTAT TATTGCAATG TGAATTGGG 5670
AACGGAAAAA TTATTTTATT AAAGAGTAGT TCAACAAACG GGCCAGTTTG 5720
15 TTGAAGATTA GATGCTATAA TTGTTATTAA AAGGATTGAA GGATGCTTAG 5770
GAAGACGAGT TATTAATAGC TGAATAAGAA CGGTGCTCTC CAAATATTCT 5820
TATTTAGAAA AGCAAATCTA AAATTATCTG AAAAGGGAAT GAGAATAGTG 5870
AATGGACCAA TAATAATGAC TAGAGAAGAA AGAATGAAGA TTGTTTCATGA 5920
AATTAAGGAA CGAATATTGG ATAAATATGG GGATGATGTT AAGGCTATTG 5970
20 GTGTTTATGG CTCTCTTGGT CGTCAGACTG ATGGGCCCTA TTCGGATATT 6020
GAGATGATGT GTGTCATGTC AACAGAGGAA GCAGAGTTCA GCCATGAATG 6070
GACAACCGGT GAGTGGAAGG TGGAAGTGAA TTTGATAGC GAAGAGATTG 6120
TACTAGATTA TGCATCTCAG GTGGAATCAG ATTGGCCGCT TACACATGGT 6170
CAATTTTCT CTATTTTGCC GATTTATGAT TCAGGTGGAT ACTTAGAGAA 6220
25 AGTGTATCAA ACTGCTAAAT CGGTAGAAGC CCAAACGTT CACGATGCGA 6270
TTTGTGCCCT TATCGTAGAA GAGCTGTTG AATATGCAGG CAAATGGCGT 6320
AATATTCGTG TGCAAGGACC GACAACATTT CTACCATCCT TGA CTGTACA 6370
GGTAGCAATG GCAGGTGCCA TGTTGATTGG TCTGCATCAT CGCATCTGTT 6420
ATACGACGAG CGCTTCGGTC TTAAGTGAAG CAGTTAAGCA ATCAGATCTT 6470
30 CCTTCAGGTT ATGACCATCT GTGCCAGTTC GTAATGTCTG GTCAACTTTC 6520
CGACTCTGAG AAATTCTGG AATCGCTAGA GAATTTCTGG AATGGGATTG 6570
AGGAGTGGAC AGAACGACAC GGATATATAG TGGATGTGTC AAAACGCATA 6620
CCATTTTGAA CGATGACCTC TAATAATTGT TAATCATGTT GGTACGTAT 6670

TTATTAACCTT CTCCTAGTAT TAGTAATTAT CATGGCTGTC ATGGCGCATT 6720
 AACGGAATAA AGGGTGTGCT TAAATCGGGC CATTGTGCGT AATAAGAAAA 6770
 AGGATTAATT ATGAGCGAAT TGAATTAATA ATAAGGTAAT AGATTTACAT 6820
 TAGAAAATGA AAGGGGATTT TATGCGTGAG AATGTTACAG TCTATCCCGG 6870
 5 CAATAGTTAC CCTTATTATC AAGATAAGAA AGAAAAGGAT TTTTCGCTAC 6920
 GCTCAAATCC TTTAAAAAAA CACAAAAGAC CACATTTTTT AATGTGGTCT 6970
 TTATTCTTCA ACTAAAGCAC CCATTAGTTC AACAAACGAA AATTGGATAA 7020
 AGTGGGATAT TTTTAAATA TATATTTATG TTACAGTAAT ATTGACTTTT 7070
 AAAAAAGGAT TGATTCTAAT GAAGAAAGCA GACAAGTAAG CCTCCTAAAT 7120
 10 TCACTTTAGA TAAAAATTTA GGAGGCATAT CAAATGAAC TTAATAAAAT 7170
 TGATTTAGAC AATTGGAAGA GAAAAGAGAT ATTTAATCAT TATTTGAACC 7220
 AACAAACGAC TTTTAGTATA ACCACAGAAA TTGATATTAG TGTTTTATAC 7270
 CGAAACATAA AACAAGAAGG ATATAAATTT TACCCTGCAT TTATTTTCTT 7320
 AGTGACAAGG GTGATAAACT CAAATACAGC TTTTAGAACT GGTTACAATA 7370
 15 GCGACGGAGA GTTAGGTTAT TGGGATAAGT TAGAGCCACT TTATACAATT 7420
 TTTGATGGTG TATCTAAAC ATTCTCTGGT ATTTGGACTC CTGTAAAGAA 7470
 TGACTTCAAA GAGTTTTATG ATTTATACCT TTCTGATGTA GAGAAATATA 7520
 ATGGTTCGGG GAAATTGTTT CCCAAAACAC CTATACCTGA AAATGCTTTT 7570
 TCTCTTTCTA TTATTCCATG GACTTCATTT ACTGGGTTTA ACTTAAATAT 7620
 20 CAATAATAAT AGTAATTACC TTCTACCCAT TATTACAGCA GGAAATTCA 7670
 TTAATAAAGG TAATTCAATA TATTTACCGC TATCTTTACA GGTACATCAT 7720
 TCTGTTTGTG ATGGTTATCA TGCAGGATTG TTTATGAACT CTATTCAGGA 7770
 ATGTGCAGAT AGGCCTAATG ACTGGCTTTT ATAATATGAG ATAATGCCGA 7820
 CTGTACTTTT TACAGTCGGT TTTCTAATGT CACTAACCTG CCCCCTTAGT 7870
 25 TGAAGAAGGT TTTTATATTA CAGCTCCAGA TCCATATCCT TCTTTTTCTG 7920
 AACCGACTTC TCCTTTTTTCG CTCTTTTATT CCAATTGCTT TATTGACGTT 7970
 GAGCCTCGGA ACCCNTATAG TGTGTTATAC TTTACTTGGA AGTGGTTGCC 8020
 GGAAAGAGCG AAAATGCCTC ACATTTGTGC CACCTAAAAA GGAGCGATTT 8070
 ACATATGAGT TATGCAGTTT GTAGAATGCA AAAAGTGAAP TCAGGATCN 8119

30 (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala	-107	-105	-100	-95
5	Leu Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala	-90	-85	-80	
	Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys	-75	-70	-65	
	Gln Thr Met Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile	-60	-55	-50	
10	Ser Glu Lys Gly Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp	-45	-40	-35	
	Ala Ala Ser Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys	-30	-25	-20	
15	Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Val Ala His	-15	-10	-5	
	Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala	1	5	10	
	Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val	15	20	25	
20	Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys	30	35	40	
	Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe	45	50	55	
25	Gln Asp Asn Asp Ser His Gly Thr His Val Ala Gly Thr Val Ala	60	65	70	
	Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala	75	80	85	
	Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln	90	95	100	
30	Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn	105	110	115	
	Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala	120	125	130	
35	Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val	135	140	145	
	Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser	150	155	160	
	Thr Val Asp Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly	165	170	175	
40	Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly	180	185	190	
	Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr	195	200	205	

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala
 210 215 220
 Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His
 225 230 235
 5 Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr
 240 245 250
 Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile
 255 260 265
 10 Asn Val Gln Ala Ala Ala Gln
 270 275

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: Amino Acid
 15 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Leu Gly Gly Pro Ser Gly
 1 5 7

(2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25 Ala Ala Ala Gly Asn Glu Gly
 1 5 7

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 30 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Thr Val Gly Tyr Pro
 1 5 6

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Trp Gly Pro Ala Asp Asp
 1 5 7

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Phe Ala Ser Gly Asn Gly Gly
1 5 7
- (2) INFORMATION FOR SEQ ID NO:8:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
Cys Asn Tyr Asp Gly Tyr Thr
15 1 5 7
- (2) INFORMATION FOR SEQ ID NO:9:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
Ser Trp Gly Pro Glu Asp Asp
1 5 7
- (2) INFORMATION FOR SEQ ID NO:10:
- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
30 Trp Ala Ser Gly Asn Gly Gly
1 5 7
- (2) INFORMATION FOR SEQ ID NO:11:
- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
Cys Asn Cys Asp Gly Tyr Thr
1 5 7
- 40 (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Trp Ala Ser Gly Asp Gly Gly
1 5 7

(2) INFORMATION FOR SEQ ID NO:13:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Cys Asn Cys Asp Gly Tyr Ala
1 5 7

(2) INFORMATION FOR SEQ ID NO:14:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Val Ile Asp Ser Gly Ile
1 5 6

20 (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Asn Asn Ser His
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

35 Ile Val Asp Asp Gly Leu
1 5 6

(2) INFORMATION FOR SEQ ID NO:17:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Asp Asp Tyr His
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Leu Asp Asp Gly Ile
1 5 6

(2) INFORMATION FOR SEQ ID NO:19:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

15 Asn Asp Asn Arg His
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Met Asp Asp Gly Ile
1 5 6

25 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Trp Phe Asn Ser His
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

40 GCGGTTATCG ACGACGGTAT CGATTCT 27

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

5 GCGGTTATCG ACAAAGGTAT CGATTCT 27

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: Nucleic Acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGTTATCG ACGAAGGTAT CGATTCT 27

(2) INFORMATION FOR SEQ ID NO:25:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCAAGACAAC GACTCTCAG GAA 23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
25 (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCAAGACAAC AGCTCTCAG GAA 23

30 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCAAGACAAC AAATCTCAG GAA 23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 42 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

5 CACTTCCGGC AGCTCGTCGA CAGTGGACTA CCCTGGCAAA TA 42

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: Nucleic Acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CACTTCCGGC AGCTCGTCGA CAGTGGAGTA CCCTGGCAAA TA 42

(2) INFORMATION FOR SEQ ID NO:30:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTAACATGAG CCTCGGCCCA GCTAGCGGTT CTGCTGCTTT A 41

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
25 (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTAACATGAG CCTCGGCCCC GCGGATGATT CTGCTGCTTT AAA 43

30 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGCAGCTCA AGCAACGATG GCTATCCTGG CAAATACCCT TCTGTCA 47

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 44 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

5 ACTTCCGGCA GCTCTTCGAA CTACGACGGG TACCCTGGCA AATA 44

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn Leu Thr Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:35:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20 Asn Leu Met Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
25 (B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Thr Ala Ser Arg Arg
1 5

30 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Thr Arg Arg Ser
1 5

(2) INFORMATION FOR SEQ ID NO:38:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Leu Ser Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

10 Leu Met Leu Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:40:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ala Ser Thr His Phe
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

25 Gln Lys Pro Asn Phe
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Arg Lys Pro Thr His
1 5

35 (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Gln Gln Gln Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
Arg Pro Gly Ala Met
1 5
- (2) INFORMATION FOR SEQ ID NO:45:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
Gln Gly Glu Leu Pro
15 1 5
- (2) INFORMATION FOR SEQ ID NO:46:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
Ala Pro Asp Pro Thr
1 5
- (2) INFORMATION FOR SEQ ID NO:47:
- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
Gln Leu Leu Glu His
30 1 5
- (2) INFORMATION FOR SEQ ID NO:48:
- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
Val Asn Asn Asn His
1 5
- 40 (2) INFORMATION FOR SEQ ID NO:49:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ala Gln Ser Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:50:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

10 Thr Ala Ser Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His His His His His His
1 5 6

20 (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Leu Met Arg Lys
1 4

(2) INFORMATION FOR SEQ ID NO:53:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

35 Leu Thr Ala Arg
1 4

(2) INFORMATION FOR SEQ ID NO:54:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Pro Gly Gly
1 4

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: Amino Acid

5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Leu Met Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: Amino Acid

10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

15 Ala Ala Pro Phe
1 4

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

20 (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Gly Pro Gly Gly Xaa Xaa Xaa Xaa Xaa Gly Gly Pro Gly
1 5 10 13

25 (2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala Ala Pro Lys
1 4

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 4 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

40 Ala Ala Pro Arg
1 4

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ala Ala Pro Met
1 4

5 (2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Ala Pro Gln
1 4

(2) INFORMATION FOR SEQ ID NO:62:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

20 Ala Ala Lys Phe
1 4

(2) INFORMATION FOR SEQ ID NO:63:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Ala Ala Phe
1 4

(2) INFORMATION FOR SEQ ID NO:64:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

35 Ala Ala Arg Phe
1 4

(2) INFORMATION FOR SEQ ID NO:65:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Ala Asp Phe

1 4

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Ala Lys Lys
1 4

10 (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Ala Lys Arg
1 4

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

25 Ala Ala Lys Phe
1 4

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ala Ala Pro Xaa
1 4

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

40 Ala Ala Xaa Phe
1 4

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5 Ala Ala Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 275 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

	Ala	Gln	Ser	Val	Pro	Tyr	Gly	Val	Ser	Gln	Ile	Lys	Ala	Pro	Ala	1	5	10	15
15	Leu	His	Ser	Gln	Gly	Tyr	Thr	Gly	Ser	Asn	Val	Lys	Val	Ala	Val	20	25	30	
	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu	Lys	Val	Ala	35	40	45	
20	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Phe	Gln	Asp	50	55	60	
	Asn	Asp	Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Ala	Leu	65	70	75	
	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	Ala	Ser	Leu	80	85	90	
25	Tyr	Ala	Val	Lys	Val	Leu	Gly	Ala	Asp	Gly	Ser	Gly	Gln	Tyr	Ser	95	100	105	
	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ala	Asn	Asn	Met	Asp	110	115	120	
30	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Ala	Leu	125	130	135	
	Lys	Ala	Ala	Val	Asp	Lys	Ala	Val	Ala	Ser	Gly	Val	Val	Val	Val	140	145	150	
	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser	Thr	Val	155	160	165	
35	Asp	Tyr	Pro	Gly	Lys	Tyr	Pro	Ser	Val	Ile	Ala	Val	Gly	Ala	Val	170	175	180	
	Asp	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Val	Gly	Pro	Glu	185	190	195	
40	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Pro	200	205	210	
	Gly	Asn	Lys	Tyr	Gly	Ala	Tyr	Asn	Gly	Thr	Ser	Met	Ala	Ser	Pro	215	220	225	
	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His	Pro	Asn	230	235	240	

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr
245 250 255

Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val
260 265 270

5 Gln Ala Ala Ala Gln
275

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Arg Val Arg Arg
1 4

15 (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1146 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTG AGA GGC AAA AAA GTA TGG ATC AGT TTG CTG TTT 36
Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe
-107 -105 -100

25 GCT TTA GCG TTA ATC TTT ACG ATG GCG TTC GGC AGC ACA 75
Ala Leu Ala Leu Ile Phe Thr Met Ala Phe Gly Ser Thr
-95 -90 -85

30 TCC TCT GCC CAG GCG GCA GGG AAA TCA AAC GGG GAA AAG 114
Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
-80 -75 -70

AAA TAT ATT GTC GGG TTT AAA CAG ACA ATG AGC ACG ATG 153
Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met
-65 -60

35 AGC GCC GCT AAG AAG AAA GAT GTC ATT TCT GAA AAA GGC 192
Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
-55 -50 -45

GGG AAA GTG CAA AAG CAA TTC AAA TAT GTA GAC GCA GCT 231
Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala
-40 -35

40 TCA GCT ACA TTA AAC GAA AAA GCT GTA AAA GAA TTG AAA 270
Ser Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys
-30 -25 -20

45 AAA GAC CCG AGC GTC GCT TAC GTT GAA GAA GAT CAC GTA 309
Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Val
-15 -10 -5

AGA CAT AAG CGC GCG CAG TCC GTG CCT TAC GGC GTA TCA 348

	Arg	His	Lys	Arg	Ala	Gln	Ser	Val	Pro	Tyr	Gly	Val	Ser	
					1				5					
5	CAA	ATT	AAA	GCC	CCT	GCT	CTG	CAC	TCT	CAA	GGC	TAC	ACT	387
	Gln	Ile	Lys	Ala	Pro	Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr	
	10					15					20			
	GGA	TCA	AAT	GTT	AAA	GTA	GCG	GTT	ATC	GAC	AGC	GGT	ATC	426
	Gly	Ser	Asn	Val	Lys	Val	Ala	Val	Ile	Asp	Ser	Gly	Ile	
			25					30					35	
10	GAT	TCT	TCT	CAT	CCT	GAT	TTA	AAG	GTA	GCA	GGC	GGA	GCC	465
	Asp	Ser	Ser	His	Pro	Asp	Leu	Lys	Val	Ala	Gly	Gly	Ala	
					40					45				
	AGC	ATG	GTT	CCT	TCT	GAA	ACA	AAT	CCT	TTC	CAA	GAC	AAC	504
	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Phe	Gln	Asp	Asn	
		50					55					60		
15	GAC	TCT	CAC	GGA	ACT	CAC	GTT	GCC	GGC	ACA	GTT	GCG	GCT	543
	Asp	Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	Ala	Ala	
				65				70						
	CTT	AAT	AAC	TCA	ATC	GGT	GTA	TTA	GGC	GTT	GCG	CCA	AGC	582
	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	
20		75				80					85			
	GCA	TCA	CTT	TAC	GCT	GTA	AAA	GTT	CTC	GGT	GCT	GAC	GGT	621
	Ala	Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Gly	Ala	Asp	Gly	
			90					95					100	
25	TCC	GGC	CAA	GAT	AGC	TGG	ATC	ATT	AAC	GGA	ATC	GAG	TGG	660
	Ser	Gly	Gln	Asp	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	
					105					110				
	GCG	ATC	GCA	AAC	AAT	ATG	GAC	GTT	ATT	AAC	ATG	AGC	CTC	699
	Ala	Ile	Ala	Asn	Asn	Met	Asp	Val	Ile	Asn	Met	Ser	Leu	
		115					120					125		
30	GGC	GGA	CCT	TCT	GGT	TCT	GCT	GCT	TTA	AAA	GCG	GCA	GTT	738
	Gly	Gly	Pro	Ser	Gly	Ser	Ala	Ala	Leu	Lys	Ala	Ala	Val	
					130				135					
	GAT	AAA	GCC	GTT	GCA	TCC	GGC	GTC	GTA	GTC	GTT	GCG	GCA	777
	Asp	Lys	Ala	Val	Ala		Gly	Val	Val	Val	Val	Ala	Ala	
35		140				145					150			
	GCC	GGT	AAC	GAA	GGC	ACT	TCC	GGC	AGC	TCG	TCG	ACA	GTG	816
	Ala	Gly	Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser	Thr	Val	
			155					160					165	
	GAC	TAC	CCT	GGC	AAA	TAC	CCT	TCT	GTC	ATT	GCA	GTA	GGC	855
40	Asp	Tyr	Pro	Gly	Lys	Tyr	Pro	Ser	Val	Ile	Ala	Val	Gly	
					170					175				
	GCT	GTT	GAC	AGC	AGC	AAC	CAA	AGA	GCA	TCT	TTC	TCA	AGC	894
	Ala	Val	Asp	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	
			180				185					190		
45	GTA	GGA	CCT	GAG	CTT	GAT	GTC	ATG	GCA	CCT	GGC	GTA	TCT	933
	Val	Gly	Pro	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	
					195				200					
	ATC	CAA	AGC	ACG	CTT	CCT	GGA	AAC	AAA	TAC	GGG	GCG	TAC	972
	Ile	Gln	Ser	Thr	Leu	Pro	Gly	Asn	Lys	Tyr	Gly	Ala	Tyr	

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	60		65		70
	Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala				
	75		80		85
5	Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln		95		100
	Asp Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn		110		115
	Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala		125		130
10	Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val		140		145
	Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser		155		160
15	Thr Val Asp Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly		170		175
	Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly		185		190
	Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr		200		205
20	Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala		215		220
	Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His		230		235
25	Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr		245		250
	Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile		260		265
	Asn Val Gln Ala Ala Ala Gln		275		

30 (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Asn Arg Met Arg Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly
 1 5 10 11

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gly Asp Ile Thr Thr Glu Asp Glu Ala Ala Ser
 1 5 10 11

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser
 1 5 10 11

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Pro Phe Met Thr Asp Ile Ile Glu Ala Ser Ser
 1 5 10 11

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Ile Val Thr Asp Ala Ile Glu Ala Ser Ser
 1 5 10 11

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTCGCGCC AAGATAGCTG GATCATT 27

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAATACAGC TGGGAAATTA ACGGAATCG 29

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 31 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

15 GGTTCGGGCC AAGATAGCTG GGAAATTAAC G 31

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: Nucleic Acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AAGAAGATCA CGTAAGACAT AAGCGCGCGC 30

(2) INFORMATION FOR SEQ ID NO:86:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

30 Arg Ala Lys Arg
1 4

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
35 (B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Lys Ala Lys Arg
1 4

40 (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

5 Gly Pro Gly Gly Leu Met Arg Lys
1 5 8

(2) INFORMATION FOR SEQ ID NO:89:

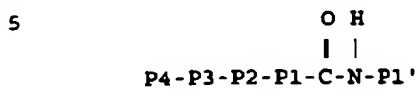
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gly Pro Gly Gly Lys Ala Lys Arg
1 5 8

What is claimed is:

1. A subtilisin variant derived from a precursor subtilisin-type serine protease said variant capable of cleaving a polypeptide substrate comprising the sequence:



wherein;

P4 is a basic amino acid;

10 P3 is any amino acid selected from the naturally occurring amino acids;

P2 is a basic amino acid;

P1 is a basic amino acid; and

P1' is not Pro.

2. The subtilisin variant of claim 1 containing an acidic amino acid at a residue equivalent to
15 Asn 62, Tyr 104 and Gly 166 of the subtilisin naturally produced by *Bacillus amyloliquefaciens*.

3. The subtilisin-type serine protease variant of claim 2 wherein the acidic amino acid is Asp or Glu.

4. The subtilisin-type serine protease variant of claim 3 wherein the acidic amino acid is Asp.

5. The subtilisin-type serine protease variant of claim 2 wherein the precursor subtilisin-type
20 serine protease in the subtilisin naturally produced by *Bacillus amyloliquefaciens*.

6. The subtilisin variant of claim 5 having the amino acid sequence of the mature polypeptide of Figure 8 (SEQ ID NO: 75).

7. A subtilisin variant having substrate specificity for peptide substrates containing dibasic amino acid sequences.

8. The subtilisin variant of claim 7 having a different amino acid residue at residue position +62
25 than subtilisin naturally produced by *Bacillus amyloliquefaciens*.

9. The subtilisin variant of Claim 8 having an Asp or Glu at residue position +62.

10. The subtilisin variant of Claim 9 having an Asp at residue position +62.

11. The subtilisin variant of Claim 10 further having an Asp or Glu at residue position +166.

30 12. The subtilisin variant of Claim 11 having an Asp at residue position +166.

13. The subtilisin variant of Claim 12 having the amino acid sequence of the mature polypeptide provided in Fig. 6.

14. An isolated nucleic acid molecule encoding the subtilisin variant of Claim 1.

15. The nucleic acid molecule of Claim 14 further comprising a promoter operably linked to the
35 nucleic acid molecule.

16. An expression vector comprising the nucleic acid molecule of Claim 15 operably linked to control sequences recognized by a host cell transformed with the vector.

17. A host cell transformed with the vector of Claim 16.

18. An isolated nucleic acid molecule encoding the subtilisin variant of Claim 7.

19. The nucleic acid molecule of Claim 18 further comprising a promoter operably linked to the nucleic acid molecule.
20. An expression vector comprising the nucleic acid molecule of Claim 19 operably linked to control sequences recognized by a host cell transformed with the vector.
- 5 21. A host cell transformed with the vector of Claim 20.
22. A process of using the nucleic acid molecule encoding the subtilisin variant to effect production of the subtilisin variant comprising culturing the host cell of Claim 21 under conditions suitable for expression of the subtilisin variant.
23. The process of Claim 22 further comprising recovering the subtilisin variant from the host
10 cell culture medium.
24. A method of using the subtilisin variant of Claim 1 comprising contacting a fusion protein containing a dibasic sequence with the subtilisin variant.
25. A process for cleaving a polypeptide, said polypeptide comprising an amino acid sequence represented by the formula:
- 15 P4-P3-P2-P1-P1'
- wherein,
- P4 is a basic amino acid;
- P3 is an amino acid selected from the naturally occurring amino acids;
- P2 is a basic amino acid;
- 20 P1 is a basic amino acid; and
- P1' is not Pro;
- comprising the step of:
- subjecting said polypeptide to the subtilisin variant of claim 1 in a reaction mixture under conditions such that the subtilisin variant cleaves the polypeptide.
- 25 26. A process of using the nucleic acid molecule encoding the subtilisin variant to effect production of the subtilisin variant comprising culturing the host cell of Claim 17 under conditions suitable for expression of the subtilisin variant.
27. The process of Claim 26 further comprising recovering the subtilisin variant from the host cell culture medium.
- 30 28. A method of using the subtilisin variant of Claim 7 comprising contacting a fusion protein containing a dibasic sequence with the subtilisin variant.
29. A process for cleaving a polypeptide, said polypeptide comprising an amino acid sequence represented by the formula:
- P4-P3-P2-P1-P1'
- 35 wherein,
- P4 is a large hydrophobic amino acid;
- P3 is an amino acid selected from the naturally occurring amino acids;
- P2 is a basic amino acid;
- P1 is a basic amino acid; and

PI' is not Pro;
comprising the step of:
subjecting said polypeptide to the subtilisin variant of claim 7 in a reaction mixture under conditions such that the subtilisin variant cleaves the polypeptide.

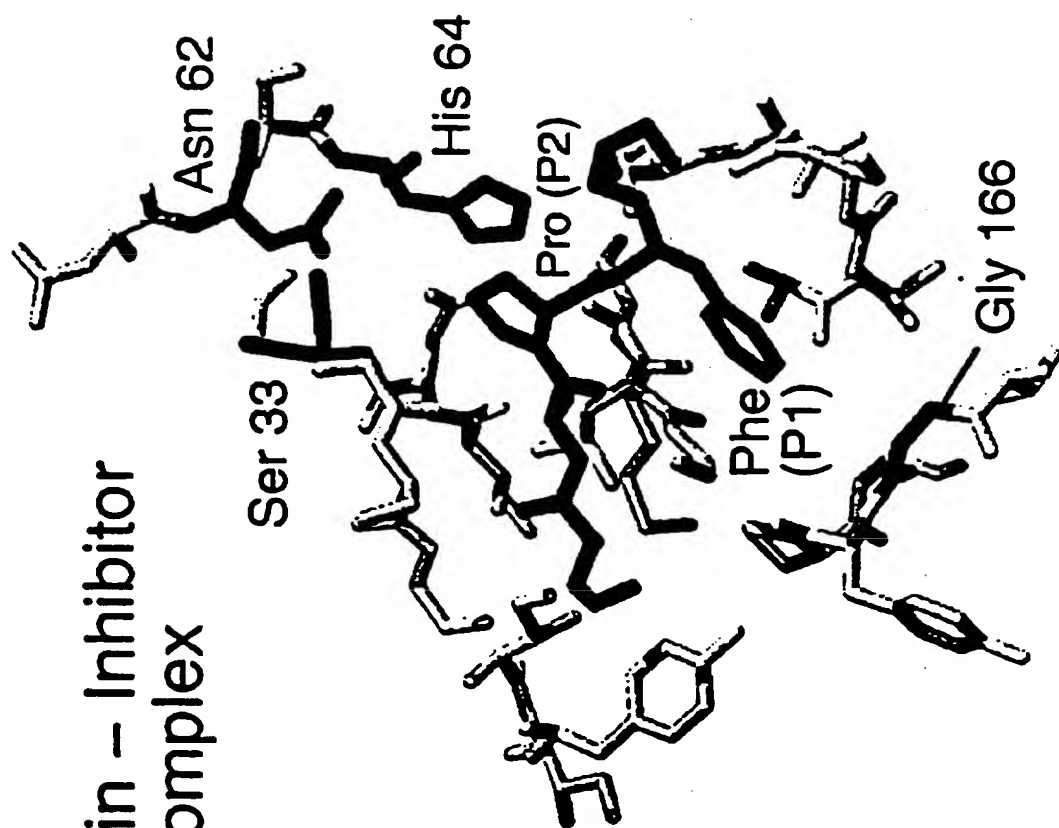


Figure 1

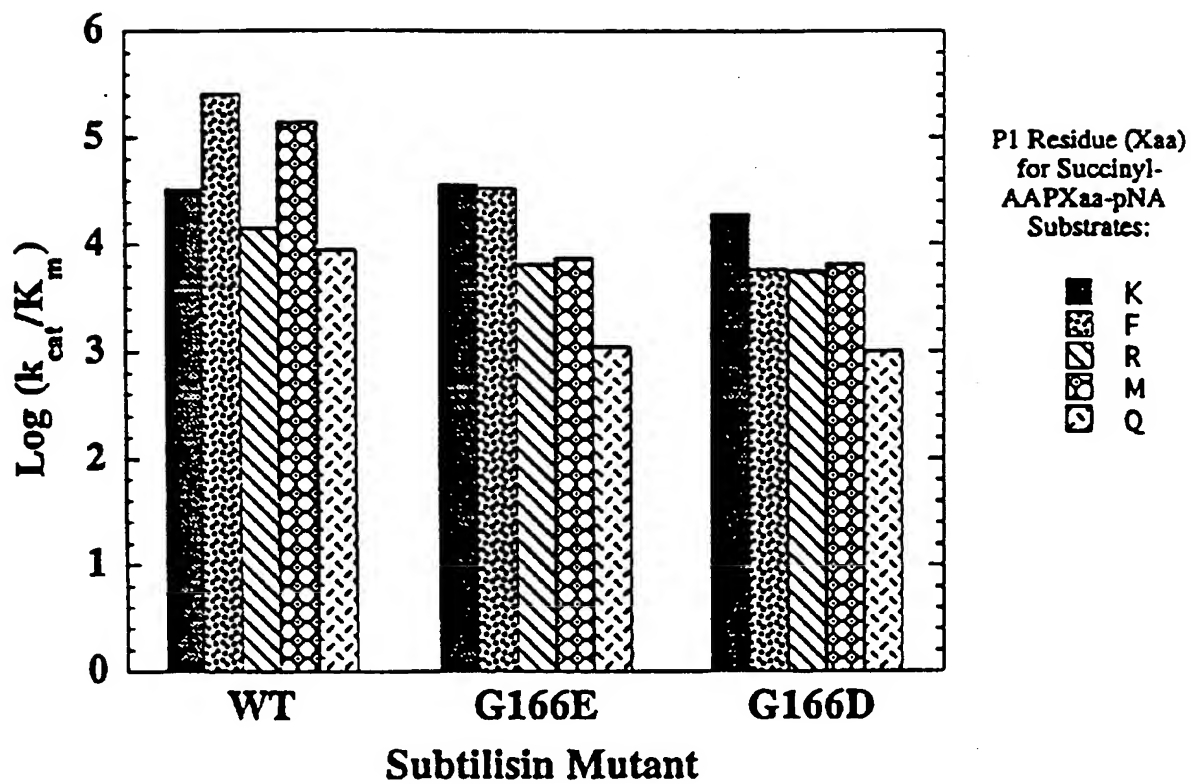


Figure 2

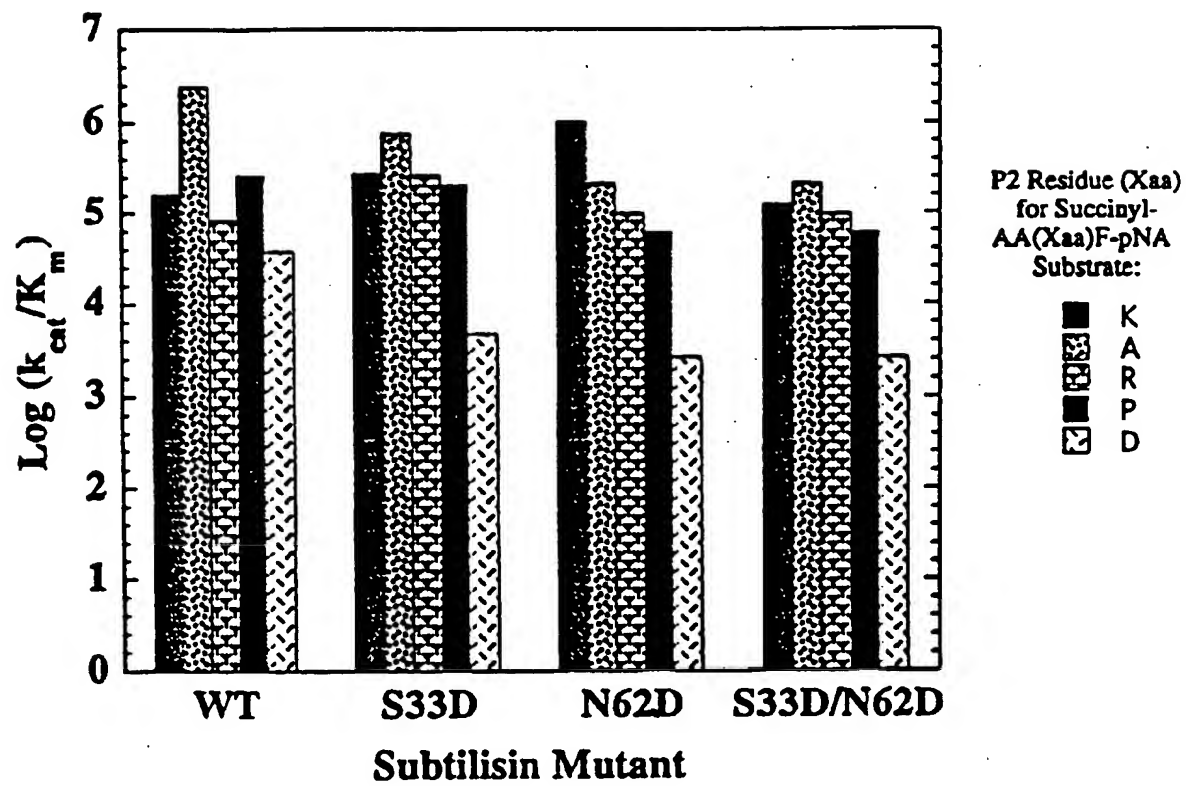


Figure 3

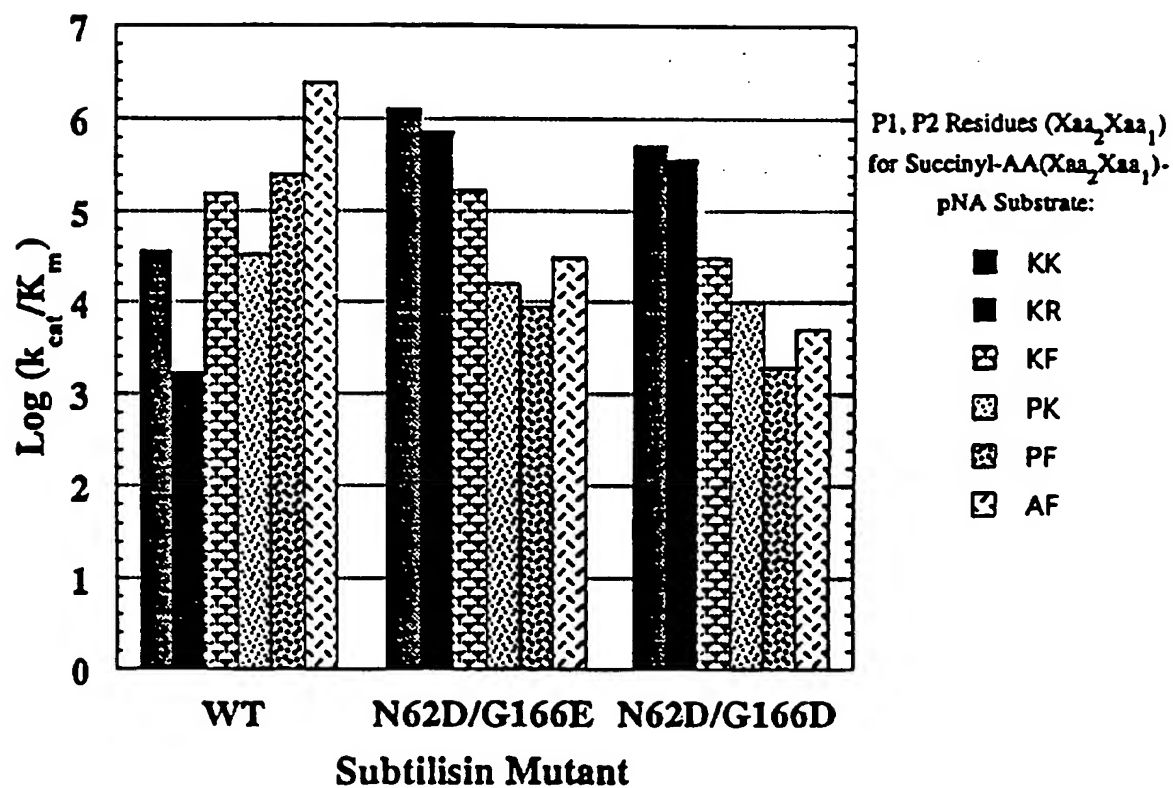


Figure 4

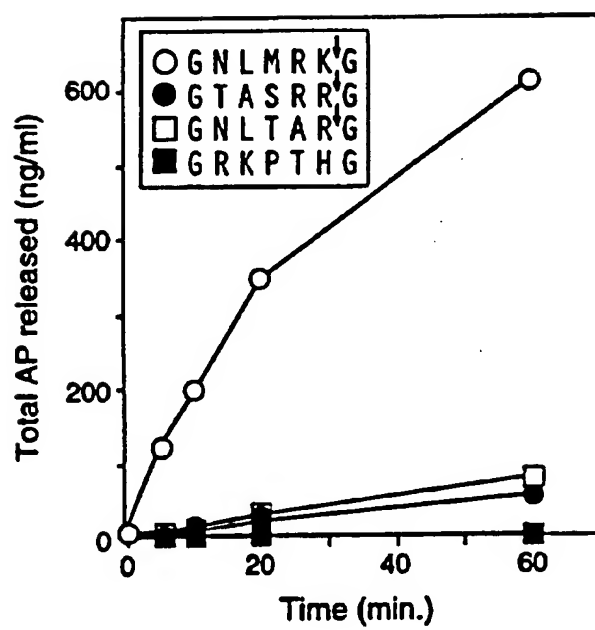


FIGURE 5

```

ecori      acci      asp1      aae1/asp1/vsp1
1  GAATTCXGGT CTACTAAAT ATTATCCAT ACTATACAT TAAATACAG AATAAATCTT CTATTCCTA TTCCTCAAT GAAATAAG AGAAGATAA
CTTAAG7CCA GATGATTTA TAAATAGCA TGAATATCTA ATTATGTCG TTAATACCA GATTAACCAAT AACAGCTTA CTTTTCCTC TCTCCATTTT

101 CA  GTG AGA GCG AAA AAA GCA TCG ATC AGT TTG CTG TTT GCT TTA GCG TTA ATC TTT ACG ATG GCG TTC GCG ACC ACA TCC
CT  CAC TCT CCG TTT TTT CAT ACC TAG TAC AAC CAC AAA CCA AAT GCG AAT TAG AAA TCG TAC GCG AAC CCG TCG TGT AGG
Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Ile Phe Thr Met Ala Phe Gly Ser Thr Ser
-100

181 TCT GCC CAG GCG GCA GCG AAA TCA AAC GCG GAA AAG AAA TAT ATT GTC GCG TTT AAA CAG ACA ATG ACC AGC AGC AGC GCG
AGA CCG GTC CCG CCG TTT AGT TTG CCG CTT TTC TTT ATA TAA CAG CCG AAA TTT GTC TGT TAC TCG TCG TCG CCG
Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala
-80

262 GCT AAG AAG AAA GAT GTC ATT TCT GAA AAA GCG GCG AAA GTG CAA AAG CAA TTC AAA TAT GTA GAC GCA GCT TCA GCT ACA
CGA TTC TTC TTT CTA CAG TAA AGA CTT TTT CCG CCG TTT CAC GGT TTC GGT ATT ATA CAT CTG CCG CCA AAT Ser Ala Thr
Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
-50

343 TTA AAC GAA AAA GCT GTA AAA GAA TTG AAA AAA GAC CCG AGC GTC GCT TAC GGT GAA GAA CAT CAC GCA GCA CAT GCG TAG
AAT TTG CTT TTT CGA CAT TTT CTT TTT CTT GCG TCG CAG CCA ATG CAA CTT CTT CTA GTC CAT CCG GTA CCG ATG
Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His Val Ala His Ala Tyr
-20

424 GCG CAG TCG GTG GCT TAC GCG GTA TCA GAA ATT AAA GCG CCG CCG GTC GAC TCT CAA GCG TAC ACT GCA TCA AAT GTT AAA
GCG GTC AGC CAC GCA ATG ATG CCG CAT AGT GGT TAA TTT CCG GCA GAC GTC AGA GGT CCG ATG TCA CCA GCT AGT TTA CAA TTT
Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
10

503 GTA GCG GTT ATC GAC AGC GGT ATC GAT TCT TCT CAT GCT GAT TTA AAG GTA GCA GCG GCA GCG AGC ATG GGT GCT TCT TCT GAA
CAT CCG CAA TAG CTG TCG CCA TAG CTA AGA AGA GTA CCA AAT TTC CAT CCG CCG CCG TCG TAC CAA GCA AGA CTT
Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu
30

586 ACA AAT GCT TTC CAA GAC AAC GAC TCT CAC GGA ACT CAC GGT GCG GCG ACA GGT GCG GCT CTT AAT AAC TCA ATC GGT GTA
TGT TTA GCA AAG GTT CTG TTG CTG AGA GTC GCT TGA GTG CAA CCG CCG TGT CAA CCG CCA GAA TTA TTG AGT TAG CCA CAT
Thr Asn Pro Phe Gln Asp Asn Asp Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val
60

```

Figure 6-1

1921 ACCAGCAGCAG CCCCCGCGCT TAATGCGCCA CTACAGGCGC CCGCCGAGC KATCCGACG CCAAGCGCGA TGGCGTCC CGTCCGCGCTT
TGGTGGGTGTG GCGCGGCGCGA ATTACGCGCG GATGTCGCGC GCAAGCGTAG TCGAGCGTGC GCGCCGCGCT ACCGAGAGG GTAATCTTA GAAGAGCGAA

2021 CCGCGGCGCAT CGGGATGGCC GCGTTCGACG CCACTCTCTC GAGGCGAGTA GATACGACC ATCAGAGCA GCTTCAGCA TCGCTCGCG CTTTACGAG
 GCGCGCGCTA GCGCTACGGG CGCAACCTCC GGTACACACAG GTCCGTCCAT CTACTCTCTG TAGTCTCTCT CCAAGTTCCT AGCGAGCGC GAGCATGGTC

haeI
 bspHI
 hgiAI/aspHI
 bspI386
 bclIKAI
 bayI
 haeI
 kaeI
 hliII/soyI
 hgiCI
 haeII
 baeI
 aheII/bsaHI

2121 CCTAAGCTCG ATCACTGACG CGTCAATGCT CAGGCGAATT TATGCGCGCT CGCGGAGCAG ATGGAACGGG TTGGCATGGA TTGTAGCGCG CCGCTATAC
 GCAATTCAGC TAGTGAAGCTG GCGACTACCA GTCCGCGTAA ATACGAGGGA GCGGCTCTCT TACCTTCCG AACCTTACT AACATCCCG GCGGGAATATG

napBII
 bglI
 hgiAI/aspHI
 bspI386
 bclIKAI
 bayI
 haeI
 kaeI
 hliII/soyI
 hgiCI
 haeII
 baeI
 aheII/bsaHI

2221 CTGTCTGCG TCCCGCGCTT GCGTCCGCGT GCATGAGCG GCGGCACTCT GAGCTTAATG GAGCGCGCG GCACCTGCGT AACGATTC ACACTCCAG
 GACGAGCGG AGCGGCGGCA CGCAGCGGCA CGTACCTCG CCGGTGAGG CTGAGCTTAC CTTGCGCGCG CGTCAAGCA TTGCTTAAGT GGTGAAGTTG

nciI
 auiII/foPI
 styI
 pfiMI
 gaeI/bpaI
 otfI01
 nseI baeI
 hgiCI

2321 AATTGGAGCG AATCAATCT TCGGAGAGC TGTCATGCG CAAGCGACC CTGGGAGAA CATATCCATC GCGTCCGCGA TCTCCAGAG CCGGACGCG
 TTAACTCTCG TTAGTTAAGA AGCGCTCTTG ACACTTACCG GTTGGTTGG GAACTCTT GTATAGTAG CCGAGCGCGT AGAGTCTCT CCGTCCGCG

nciI
 auiII/foPI
 styI
 pfiMI
 gaeI/bpaI
 otfI01
 nseI baeI
 hgiCI

2421 GCGATCTCG GCGGCTTCG TCGCTTTT GCATAGGCTC GCGCGCGCTG AGGAGCATCA CAAATATCA GCGTCAAGTC AGAGTGGCG AAACCGGCA
 GCGTAGAGC CGCGCGAGC AGCGCAAAA GGTATCCGAG GCGGAGGAG TCGTCTGAT GTTTTACT GCGAGTTGAG TCTCCAGCG TTGGGCTGT

nciI
 auiII/foPI
 styI
 pfiMI
 gaeI/bpaI
 otfI01
 nseI baeI
 hgiCI

2521 GCACTATATA GATACGAGC GTTCCCGCT GGAAGCTCG TCGTGGCTC TCGTGTTCG ACCCTGCGCG TTACCGGATA CCGTCTCGCG TTTCTCCCT
 CCGATATTT CTATGCTCG CAAGGCGGA CTTTCAGGG AGCAAGCGAG AGCAAGAGCG TCGGACGCGG AATGCGCTAT GGAACAGGCG AAAAGCGGA

haeI
 bspHI
 hgiAI/aspHI
 bspI386
 bclIKAI
 bayI
 aheII/bsaHI
 aheII/soi

2621 CCGGAGCGCT GCGGCTTCT CAATCTCAG GCTGAGGTA TCTCAGTTG GTATAGTGG TTGCTTCGA GCTGGAGTGT GTGCAGAGC CCGCGCTCA
 GCGCTTCGA CCGCGAAGA GTTACGAGTG CGACATCAT AGAGTACAG CACATCCAG AACGAGGT CGACCGGCA CAGTCTTG GCGGCGAAGT

haeI
 bspHI
 hgiAI/aspHI
 bspI386
 bclIKAI
 bayI
 aheII/bsaHI
 aheII/soi

2721 GCGGAGCGCT TCGGCTTAT CCGGTAACTA TCGTCTGAG TCGAACCGG TAAGAGAGCA GTTATCGCA CTGGGAGGAG CCACTCGTAA CAGATTAC
 CCGGCTGCG AGCGGAAATA GCGCATTAAT AGCAAGATC AGCTTGGCC ATTCTGCT CAATAGCGCT GACGCTGCT GTGACCAAT GTCTAATG

nciI
 auiII/foPI
 styI
 pfiMI
 gaeI/bpaI
 otfI01
 nseI baeI
 hgiCI

Figure 6-4

10/17

Figure 6-5

3721 GTGATGCCAT CCGTAACATG CTTTCTGTG ACTGTGAGT ACTCAACCA GTGATTCTGA GAAATAGTGA TGGCGCGACG GAGTTGCTCT TCGCCGCGCT
CAGTACGGTA GGCATTCTAG CAACAACAC TCACCACTGA TGAATTGCT CAGTAAGACT CTATTCACAT AGCGCGCTGG CTCAACGAGA ACGGCGCGCA

3821 CAACACGGCA TAATACCGCG CCACATAGCA GAACCTTAA AGTGTGATC ATTGAAAC GTTCTCGCG CGCAAACTC TCAAGAGTCT TACCGCTGT
CTTGTGCGCT ATTATGCGCG GGTGTATGCT CTCAAAATT TCACAGTAG TAACCTTG CAACAGCCG CGCTTTAG AGTCTGAGA ATGCGCACA

3921 GAGATCCAGT TCGATGTAC CCACTGTGC ACCCACTGA TCTTACGAT CTTTACTTT CACCAAGCTT TCTGCGTAG CAACAACAG AAGCAAAAT
CTCTAGGTCA AGCTACATTC GGTGACGAC TCGGTGACT AGAAGTCGA GAAATGAA GTGTGCGCA AGACCCACTG GTTTCTGC TTCCGTTTA

4021 GCCGCAAAA AGCAATAG GCGCACGCG AATGTGA TACTGATAG CTTCCTTTT CAATATTAAT CAACGATTA TCAGGCTAT TGTCTGATG
CGCGCTTTT TCCCTATTG CCGGTGCGC TTACAACTT ATGAGTATGA CAACGAAA GTTAATATA CTTCGTAAT AGTCCATA ACAAGTACT

4121 GCGGATACAT ATTGAATGT ATTAGAAA ATAAACAAT AGGGGTTCCG CGCACTTTC CCGCAAAAGT GCGACCTGAC GTCTAAGAA CCAATTAAT
CGCCTATGTA TAACTTACA TAACTTTT TATTGTTTA TCCCAAGGC GCGGTAAAG GGGCTTCA CGGTGACTG CAGATCTTT GGTATATA

4221 CATGACATTA ACCATATAA ATAGCGGAT CACCAAGCCG TTTCGTCTTC AAGCAATTAAT TCTTAAAGCA ACCTACAGAC GCGTTAAAG CTTTAAAA
GTACTGTAA TCGATATTAT TATCCGATG GTCTCGCGG AAGCAAGAG TTCTTAATTA AGCAATTCCT TGCATGTCTG CCGAATTTG GGAATTTT

4321 CGTTTATAG GGGTTGTAG ACAAGTAA GATTAACA GCAAAATTC AAGAAAACA CGATTAGCA CTTAAAAA AGCAATTGA ACTAAGCAT
GCAAAATTC CCAAAACAT TGTTCATTT CCAATTTCT GCGTTAAG TTCTTTCT GCTAAATCTT GCAATTTCT TCTTAACCT TGAATCAGTA

3721 *scd1*
mer1
hog1
hml1/aoi1
hml1/bsh1

3821 *hgl1/aspH1*
bap126
bshKAI
pep14061
xmi1
asp700
bely1/xho1
aspB1

3921 *bely1/xho1*
alv411/sno1
eco571
ase1/sno1
bmy1
ase1/sno1
eco571
ase1/kep6321
asp1
rcal
bapH1
barB1

4021 *ase1/kep6321*
asp1
rcal
bapH1
barB1

4121 *hml1/aoi1*
hml1/bsh1
atli1
rcal
bapH1

4221 *bpuA1*
bbs1
xmi1
ase1/asn1/vep1
eco1091/drai1
asp700
af111/bcf1
pep14061
ahai11/drai1

4321 *spo1*

12/17

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4421 AACCGAGAGC TAAGAAAAGA ACGAAGTGA GATCAGGGA TGAGTTATA AATAAANA AGCACTGA AACGTGCT TTTTGATGG TTTGAACTT
TTGGCTCTCC ATTTTTCCT TCCTCAGCT CTAAGTCCCT ACTCAAAATAT TTAATTTTTC TCGTGAGCTT TCCACAGAA AAAAAGTACC AAAAGTTGAA
XbaI
asp700

4521 GTTCCTTCTT ATCTGATAC ATATAGAAAT AACGTCAATT TTAATTAGT TGCTGAAGG TCGCTGAAG TGTGGATAG TATGTGTTT AAAGTATGA
CAAGAAAGAA TAGAACTATG TATATCTTTA TTGCACTAA ATTAATAATCA AGCACTTCC AGCGAACTTC ACAACCAATAC ATACACAAA TTTCAATAC
XbaI/draI

4621 AAACCTTAA AATTGGTGC ACAGAAAAC CCGATCTGTT AAAGTTATA GTCACTAAC AAATACATA ATAGATGGG GTTCTTTT AATATATGT
TTTGGGAATT TTAACCAAGC TGTCTTTTG GGGTAGACA TTTCAATATTT CACTGATTTG TTAATGATT TATCTACCC CAAAGAAAT TATAATACAC
XbaI
styI
ncol
bsaI dsaI

4721 TCCTAATAGT AGCAATTAT CAGATGAAA ATCAAGGCTT TTAGTGACA AGCAAAAAG TCGAAAAGT AGACCAATGA GAGAAAGAA AATCGCTAT
AGGATTATCA TCGTAATTA GTCTACTTTT TACTGCCAA ATCACTGT TGTGTTTC ACCTTTTAC TCTGTACTCT GTCTTCTT TTAGCAATTA
XbaI/draI

4821 GTTGATTACT TTCAAGTCT GCATATCTT GAATTAAA AGCGTGAAG AGTAAAGAT TCGCTGAAA TATACAGTA TAAACAAAT CGTGAACAG
CAACTAATGA AACTGAAGA CGTATAGAA CTAAATTT TCCGACTTC TCAATTCTA ACAAGACTT ATAAATCAT ATTGTTTA GCACTTCTC
XbaI
aspI

4921 GCGAAGAAA GTTGATGCA GTGTGTTT GTAAATCCAG GCTTGTCGA ATGTGCAACT GAGAGAGAGC AATGAACAT GGCATTGAG CACAAAAGT
CGCTTCTTT CACATAGCT CACACAAA CATTAGGTC CGAAACAGT TACACGTGA CCTCTCTCG TTAATTGTA CCGTAAGTCA GTGTTTCCA
XbaI
gaul/dpmI
bsaI

5021 TGTGCTGAA GTTATTAAG AAAAGCCAG AGTTCGTTG TGTCTTCCA CATTACAGT TAAAAATGTT TATGATGCG AGAATTAA TAAGGTTG
XbaI
ecor57I
ACAAAGACTT CAATTAATTTG TTTTCGTTG TCAAGCAACC ACAAAAGAT GTAAATGCA ATTTTACAA ATACTACCG TCTTAATTT ATTCTAAC
XbaI
aseI/asnI/vspI

5121 TCAGATATGG CTCAGAGATT TCCCGCAATG ATCCAAATTA AAAAATTA TAAATCTT GTTGCTTTA TCGCTGCAC GGAAGTGA ATAAATATA
AGCTATATAC GAGTTCCTAA AGCGGCTTAC TACCTATAT TTTTAAAT ATTTTGA CAACCAAAAT ACCACGTTG CCTTCACTGT TATTAATAT
XbaI
aspHI
aspHI
PvuIOI
nslI/avaIIII

5221 AAGATAATTC TTATAATCAG CACATGCTAG TATTGGATAG TGTGAACCA ACTTAATTTA AGAATACAG AAAGTACGT AATCAAAAC AATGATTCA
TTCATTAAG AATATTAAGT GTGATGCTAC ATAACTATAC ACACCTGCT TCAATAAAT TCTTATGCT TTAGATGAC TTAGTTTG TACCTAAGT
XbaI
bsaI

```

Figure 6-7

5321 ATTGGAAA AAGCAATGA ATTAGACTA TGATCCAAAT GTAAGAGTC AATGATTCG ACCGAAAT AATATAAAT CGGATATACA ATCGCAATC
 TAAACCTTT TCCGTTACT TTATCTGAT ACTAGGTTTA CATTTCGAG TTACTAGG TCCCTTTTA TTATATTTA GCGTATATCT TACCGCTTAA
 ncf1
bun1

5421 GACGAAATCG CAATAATATCC TGTAAGCAT ACGCATTTTA TGACCGATCA TGAAAGAAAG AATTGAAAC GTTGCTCTGA TTGACAGAA GCTTACACC
 CTGCTTTGAC GTTTATATAG ACAATTCCTA TCCCTAAAT ACTGGCTACT ACTCTTTTC TTAACCTTC CAACAGACT AACCTCTCT CCAATCTCG
 apo1
pdp14061

5521 GTAAAGGTT AATCTCTAT GGTGCTTGT TAAAGCAAT ACATTAATAA TTAACCTTC ATGACACAGA ACAAGCCAT TTGATTGATA CAGATGATA
 GATTTCCAA TTAGAGGATA GCACCAACA ATTTCCTTA TGATTTTTT AATTGGAAC TACTGTGCT TCTCCGCTA AACATGAT GTTACTACT
 apo1
pdp14061

5621 CGAAGAACCC GATGACATG GATTTGCTAT TATTCGAAATG TGCAATGCG AACGAAATA TTATTTAT TAAAGTAGT TCAACAAAC GCCGATTCG
 GCTTTTCGG CTACTCTAC GTAAAGATA ATACGCTAC ACCTTAACC TTCCCTTTT AATAAATAA TTCTCATCA AGTTGTTTC CCGCTAACC
 hg141/asph1
bep1286
belHKAT
bwy1
apo1

5721 TTGAGATTGA GATGCTATTA TTGTTATTA AAGATTGAA GCACTCTTAG GAAAGCAAT TATTAATAGC TGAATAGAA CCGTCTCTC CAATTTCT
 AACTCTAAT CTACGATAT ACAGAAAT TTGCTACTT CCTACGAAT CTCTCTCTA ATAAATATCG ACTTATCTT GCCACGAGG GTTATAGAA
 bpuat
bbs1
ase1/asn1/vsp1
bwy1
apo1

5821 TATTAGAAA AGCAATCTA AATTATCTG AAGAGCAAT GAGATAGTG AATGACCAA TAAATATGAC TAGAGAGAA ACAATGACA TTCTCATCA
 ATAAATCTTT TCGTTAGAT TTAAATAGAC TTTCCTCTA CTCTATGAC TTACCTGGTT ATTATAGTC ATCTCTCTT TCTTACTCT AACAGTACT
 foal
bepH1

5921 AATTAGCAA CGAATATTCG ATAAATATCG GCAATGATTT AAGCTATTC GTGTTATCG CTCTCTTGT CGTCAAGTC ATGCGGCTA TTCCGATAT
 TTAATTCCTT GCTTAATACC TATTTATAC CCACTACAA TTCCGATAC CACAAATAC GCAGAGCA GCACTCTGAC TACCGCGAT AACCTATTA
 sepi
cfr101
baw1
ase1
apo1
ken1
ear1/sep621
asp700

6021 GACATGATCT GTGCTATCTG AACAGAGCA GCAGACTTCA GCCATGAATG GACAAAGCCG CAGTGAAGC TGCAAGTGAA TTITGATAG GAAAGATTC
 CTCTACTACA CACAGTACAG TTCTCTCTT CGTCTCAAGT CGCTACTTAC CTGTGGCCA CTACCTTCC ACCTTCAGT AAACATATCG CTCTCTAAG
 bnc11/hind11
apo1
pdp14061

6121 TACTAGATTA TGCACTCTGAC GTGCAATGAC ATGCGGCTT TACAGATCT CAATTTTCT CTATTTTCC CATTATGAT TGACGCTGAT ACTTAGAAA
 ATGATCTAAT ACGTAGATC CACCTTAGTC TAACGAGCA ATGCTAGCA GTAAAGAA GATAAAGG GTAAATAGTA AGTCAAGCTA TGAATCTCT
 pdp101
nall/avall1
cfr1
ase1

Figure 6-8

6321 AGTGTATCAA ACTGTAAAT CGGTAGAGC CCAAGCTTC CAGATGCCA TTGTGCGCT TATCGTAGA GACCTGTTG AATATGACG CAATGCGCT
 TCACATAGTT TGACGATTT GCCATCTTCG GCTTGCAAG GTGCTACCGT AAACAGGGA ATAGCATCT CTCGACAAAC TTATACGTCC GTTACCGCA

bsp14061
 bsp1286
 bsp1
 ear1/ksp6321

6321 AATATTCGTG TGCAGAGAC GACACATTT CTACCATCTT TGACTGTACA GGTACGATG GCAGCTGCCA TGTGATTTG TCTGCATCAT GCGATCTGT
 TTATAGGAC ACCTTCCTCG CTGTGTAA GATGTAGGA ACTGACATGT CCACTGTTAC CGTCAAGGT AGACTAAC AGACGTAGTA GCGTAGACA

bsp1
 bsp14071
 bsp1
 bsp1
 hgi1
 ban1

6421 ATAGGACGAG CGCTTCGCTC TTAACTGAG CAGTTAAGCA ATGACATCTT CCTTACAGTT ATGACCATCT GTCCAGCTC GTATGTCTG GTCACTTC
 TATGCTGCTC GCGAAGCCAG AATTGACTTC GTCAATCTCT TATCTAGA GGAAGTCCA TACTGGTAGA CACGCTAAG CATTACAGAC CAGTGAAG

hae1
 eco47111
 bcl1
 bcl1
 bcl1
 hinc11/hind11

6521 GCACTCTGAG AACCTCTCG AATGCTACA GAATTCCTG AATGGATTC AGGAGTGAC AGAAGGACAG GGAATATAG TCGATGTCT AAAAGCATA
 GCTGAGACTC TTGCAAGAC TTACGATCT CTAAAGAC TTACCTAAG TCTGACCTG TCTGCTCTG CTAATATATC ACCTACACAG TTTCGGTAT

apo1

6621 CCATTTTGA CCAAGACTC TAATATTTT TAATCATCTT GGTACGCTAT TTATTAAGTT CTCTAGATAT TACATTAAT CATGCTCTC ATGGCGATT
 GGTAAACTT GCTACTGAG ATTATTAACA ATTAGTACA CCAATGCATA AATTAATCA GAGATCATTA ATCATTAATA GTACGACAG TACCGCTAA

sba1
 bsa1
 aae1/ae1/vsp1
 aae1/ae1/vsp1

6721 AACGGAATGA AGGCTGTCT TAAATCGGC CATTTGCT AATTAAGAAA AGCATTAAT ATGAGCGAAT TGAATTAATA ATAGCTAAT AGATTAGAT
 TTGCTTAAT TCCACACGA ATTAGCCCG GTAAAGCGA TTATCTCTT TCTAATTA TACTGCTTA ACTAATTAAT TATTCATTA TCTAATGTA

aae1/ae1/vsp1
 aae1/ae1/vsp1

6821 TAGAATAATGA AAGGGAATT TATGCTGAG AATGTACAG TCTATCCCG CAAATAGTAC CCTAATATC AAGATAGAA AGAAGAGAT TTTCGCTAC
 ATCTTTACT TTCCTCTAA ATACGCACTC TTACAATCTC AGATAGGCG GTTATCAATG GGAATATAG TCTAATCTT TCTTCTCTA AAAAGCATG

sha111/dra1

6921 GCTCAATGC TTAAATAAA CACAAAGAC CACATTTT AATGTGCTT TTAATCTCA ACTAAGCAC CCATTAAGTC AACAAAGAA AATGAGATA
 CGAGTTAGG AATTTTTT GTGTTCTG GTGTAAAA TTACACGCA AATTAAGAT TCAATTCGTG GGTATCAAG TTGTTGCTT TTAACCTAT

sha111/dra1

7021 AGTGGCATAT TTAAATAA TATATTAATG TACAGCTAAT ATGACCTTT AAAAAGAGT TGAATCTAAT GAAGAAGCA GACAGTAGC CCTCTAAT
 TCACCTATA AATTTTAT ATATAATAC AATGTCTTA TACTGAAG TTTTCTTA ACTAAGATTA CTGTTCTGT GTGTCATTC GAGCATTTA

sha111/dra1
 bsp1
 sha111/dra1
 apo1

7121 TCACTTTAGA TAAATAATTA GAGGCAAT CAAATGACT TTAAATAAT TCAATTAAG AATTCAGCA GAAAGAGAT ATTAATCAT TATTCAGAC
 AGTAATCT ATTTTAAT CCTCGTATA GTTACTGA AATTAATTA ACTAATCTG TTAACCTCT CTTCCTCTA TAAATAGTA ATAACTGG

apo1
 aae1/ksp6321

Figure 6-9

7221 AACAAACGAC TTTAGTATA ACCAGAAA TTGATATTAG TGTATTATAC CGAAACATTA AACAGACG ATATAAATTT TACCGTCAT TTAATTGCT
TTGTTTGCTG AAATCATAT TCGTCTCTTT AACTATAAC ACAAAATATG GCTTGATTT TGTCTCTCC TATATTAAA ATGCAAGCTA ATTAAGAAA

7231 AGTACACAGC GTGATTAACCT CAATATACAGC TTTTGAACCT GGTATACAATA GCGACGGAGA GTTAGCTTAT TCGCATATAGT TAGAGCCAGT TTAATCAATT
TCAGTGTCC CAGTATTGCA GTTATATCTG AAATCTTCA CCAATGTTAT GCGTCCCTCT CAATCCAAAT ACCCTATTCA ATCTCGGTCA AATATGTTAA

7421 TTTCATGCTG TATCTAAAC ATTCCTGCT ATTGGAATC CTGTAAAGAA TGACCTCAAA GAGTTTATG ATTATATACCT TTCTCATGTA GAGAAATATA
AAACTACCAAC ATACATTTTG TAAGACAGCA TAAACCTGAG GACATTTCTT ACTGAAGTTT CTCAAAATATC TAAATATGCA AAGCTACAT CTCTTAATAT

7521 ATGCTTCGGG GAAATGCTTT CCCAAACAC CTATACCTGA AAATGCTTT TCTTTCTA TTATTCATG CACTTCATTT ACTGCGTTA ACTTAAATAT
TACCAAGCCC CTTTAAAGAA GCGTTTCTG GATATGCACT TTACGAAA AGAGAAAGAT AATAGCTAC CTGAATTA TACCCAAAT TGAATTATA

7621 CAATTAATAT AGTAATTACC TTCTACCCAT TATTACAGCA GGAATATCA TTAATTAAGC TAAATCAATA TATTACCCG TATCTTACA GGTATCATAT
GTATTATTAT TCAATTAATG AGATCGCTA ATATGTCGT CCTTTAAGT AATATTTCC ATTAAAGTAT ATAAAGCGC ATCAAAATGT CCAATGATGA

7721 TCTGTTGCTG ATGCTATCA TCGACGATTG TTTATGAACT CTATTCAGCA ATTGTCAGAT AGCGCTATAG ACTGCGTTT ATTAATATGAG ATAAAGCCGA
AGACAAACAC TACCAATATG ACGTCTTAC AAATACCTGA GATAGTCTT TACAGTCTA TCGGATTAAC TGACGAAA TATTATATCTG TATTACGCGT

7821 CTGTACTTTT TACAGTCGGT TTCTAATGT CAGTAACTCG CCGCGTATG TGAAGAAAGT TTTATATTA CAGCTCCAGA TCGATATCGT TCTTTCTG
GACATGAAA ATGTACGCCA AAGATTACA GTGATTTGAC GGGCAATCA ACTCTTCCA AAAATATAT ATCGAGGCT AGGTATAGCA ACATAAAGAC

7921 AACGACTTC TCGTTTTCG CTTCCTTATT CGAATTCGCT TATTGACGCT GACCTCGCA ACCGXTATAG TGTGTTATAC TTTACTTGA AGTGGTTGCG
TTGCGCTGAG AGGAAAGAC GAAAGAAATA GGTATAGCA ATAACTGCA CTGCGAGCT TCGGTATATC ACAGAAATAG AATGAACTG TACCAAGCG

8021 GGAAGAGCG AAATGCTCT ACATTTGCTC CACCTAATA GAGCGGATTT ACATATGAGT TATGACGTTT GTACATGCA AAAAGTGAA TCAAGATCX
CCTTCTGCG TTTACCGAG TGTAAACAGC GTGATTTT CCTCGCTAAA TGTATCTCA ATACGCAAA CATTACGT TTTGACCTT AGTCTAGT

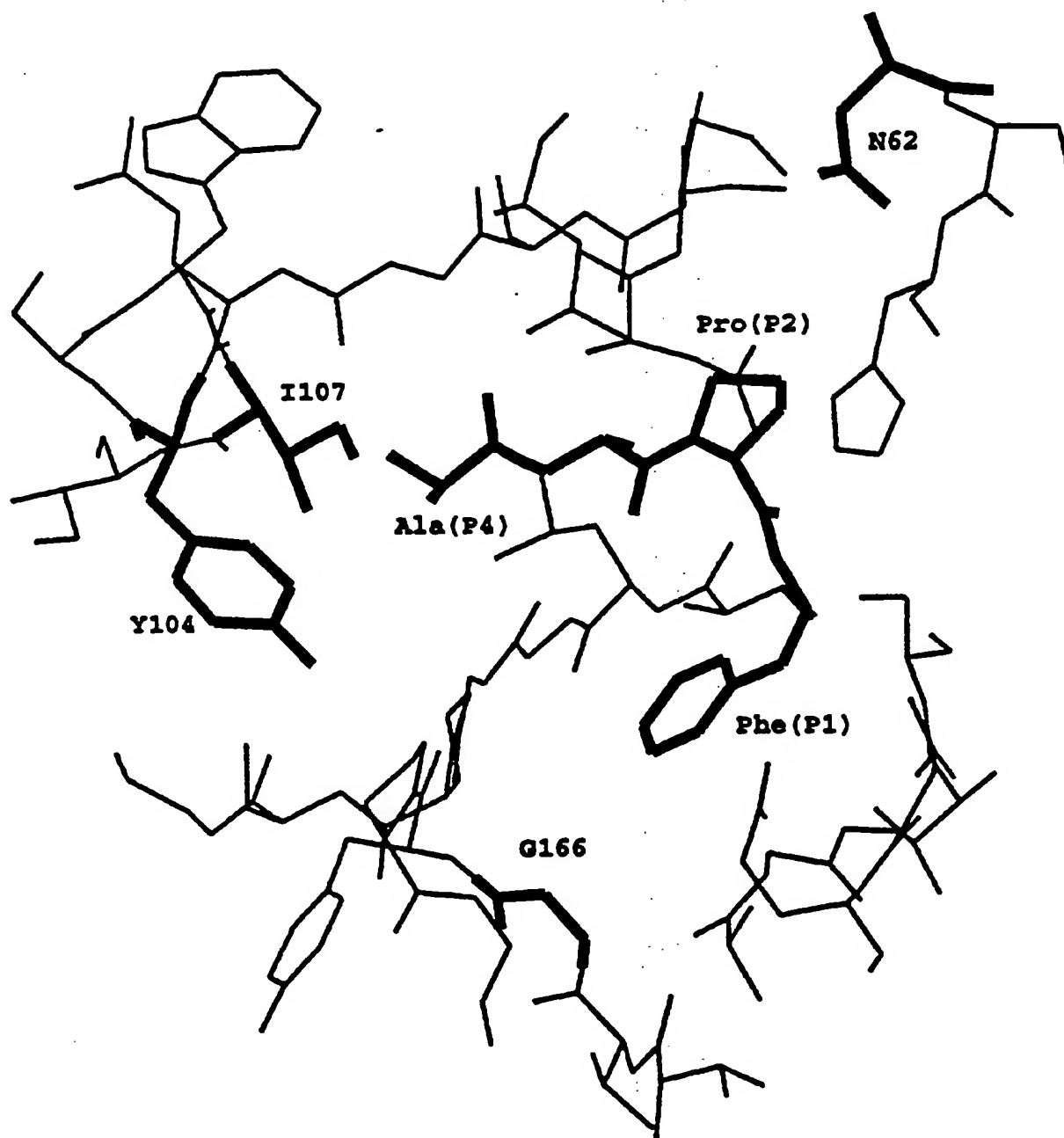


FIGURE 7

Val	Arg	Gly	Lys	Lys	Val	Trp	Ile	Ser	Leu	Leu	Phe	Ala	Leu	Ala
-107	-105						-100					-95		
Leu	Ile	Phe	Thr	Met	Ala	Phe	Gly	Ser	Thr	Ser	Ser	Ala	Gln	Ala
	-90						-85					-80		
Ala	Gly	Lys	Ser	Asn	Gly	Glu	Lys	Lys	Tyr	Ile	Val	Gly	Phe	Lys
	-75						-70					-65		
Gln	Thr	Met	Ser	Thr	Met	Ser	Ala	Ala	Lys	Lys	Lys	Asp	Val	Ile
	-60						-55					-50		
Ser	Glu	Lys	Gly	Gly	Lys	Val	Gln	Lys	Gln	Phe	Lys	Tyr	Val	Asp
	-45						-40					-35		
Ala	Ala	Ser	Ala	Thr	Leu	Asn	Glu	Lys	Ala	Val	Lys	Glu	Leu	Lys
	-30						-25					-20		
Lys	Asp	Pro	Ser	Val	Ala	Tyr	Val	Glu	Glu	Asp	His	Val	Arg	His
	-15						-10					-5		
Lys	Arg	Ala	Gln	Ser	Val	Pro	Tyr	Gly	Val	Ser	Gln	Ile	Lys	Ala
	1					5					10			
Pro	Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr	Gly	Ser	Asn	Val	Lys	Val
	15					20					25			
Ala	Val	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu	Lys
	30					35					40			
Val	Ala	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Phe
	45					50					55			
Gln	Asp	Asn	Asp	Ser	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	Ala
	60					65					70			
Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro	Ser	Ala
	75					80					85			
Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Gly	Ala	Asp	Gly	Ser	Gly	Gln
	90					95					100			
Asp	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ala	Asn	Asn
	105					110					115			
Met	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Ala
	120					125					130			
Ala	Leu	Lys	Ala	Ala	Val	Asp	Lys	Ala	Val	Ala	Ser	Gly	Val	Val
	135					140					145			
Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Thr	Ser	Gly	Ser	Ser	Ser
	150					155					160			
Thr	Val	Asp	Tyr	Pro	Gly	Lys	Tyr	Pro	Ser	Val	Ile	Ala	Val	Gly
	165					170					175			
Ala	Val	Asp	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Val	Gly
	180					185					190			
Pro	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr
	195					200					205			
Leu	Pro	Gly	Asn	Lys	Tyr	Gly	Ala	Tyr	Asn	Gly	Thr	Ser	Met	Ala
	210					215					220			
Ser	Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His
	225					230					235			
Pro	Asn	Trp	Thr	Asn	Thr	Gln	Val	Arg	Ser	Ser				

INTERNATIONAL SEARCH REPORT

International Application No

PC./US 96/02861

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/57 C12N9/54 C12N1/21 C12P21/06

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	R. SIEZEN ET AL: "Homology modelling and protein engineering strategy of subtilases, the family of subtilisin-like serine proteinases" see the whole document especially figure 3, table V and page 729, right column, last paragraph-page 730 and Discussion --- -/--	1-29

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

18 July 1996

Date of mailing of the international search report

31.07.96

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INTERNATIONAL SEARCH REPORT

International Application No

PC./US 96/02861

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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INTERNATIONAL SEARCH REPORT

International Application No

PC./US 96/02861

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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P,Y	--- KEYSTONE SYMPOSIUM ON PROCESSING ENZYMES: BIOCHEMISTRY, GENETICS AND CLINICAL RELEVANCE, LAKE TAHOE, CALIFORNIA, USA, MARCH 2-8, 1995. JOURNAL OF CELLULAR BIOCHEMISTRY SUPPLEMENT 0 (19B). 1995. 233. ISSN: 0733-1959, 4 March 1995, XP002008741 WELLS J A ET AL: "Subtilisin: An enzyme made for engineering." see abstract B7-012 -----	1-29

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PC./US 96/02861

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		WO-A-	9100335	10-01-91
		JP-T-	4500384	23-01-92

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